Mouse ELAC2 cDNA. Chemically treated Signal transductio

Human metastasis a Human gene regulat immune syste

Chemically treated

Genomic sequence # Neisseria meningit

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Human

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DNA encoding novel Human prostate can

Novel human coding

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Human; prostate cancer predisposing gene; HPC2; chromosome 17p; gene therapy; peptide therapy; drug design; ds.
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/transl_except= (pos:23892..23895,aa:Glu)
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                                                               ABL70151
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10110.387 Million cell updates/sec
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                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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S. epidermidis gen Plasmodium var-7 g Plasmodium var-7 p

cDNA sequence #583

Staphylococcus epi

Drosophila melanog

cDNA encoding

DNA transcription

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The present sequence is the genomic sequence of the human prostate cancer predisposing gene HPC2, which is found on chromosome 17p. Some alleles of this gene cause a predisposition to cancer, particularly prostate cancer. This gene and its protein can be used in peptide and gene therapy for cancer patients, as well as being useful as diagnostic tools (both for cancer sufferers and those with a predisposition to the disease) and in the production of cancer drugs. This sequence was isolated by cloning and sequencing the region of the genome which appeared to cause a predisposition to prostate cancer.
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100.0%; Pred. No. 6.4e-222;
.ive 0; Mismatches 0; Indels
                Rommens JM;
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              Simard J,
                Tavtigian SV, Teng DHF,
                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 801; Conservative
                                                WPI; 2000-376481/32
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prostate cancer predisposing gene.
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(HOSP-) HOSPITAL FOR SICK CHILDREN.
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Matches 801;
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                                                                                                                                                                                                   Human; immune; haematopoietic; immune/haematopoietic antigen; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                              Human immune/haematopoietic antigen genomic sequence
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2000US-0241785. 2000US-0241786. 2000US-0241786. 2000US-0249209 2000US-0249214 2000US-0249264 13-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 10-NOV-2000; 08-NOV-2000; 17-NOV-2000; 05-JAN-2001; 17 - NOV - 2000; 7-NOV-2000;

Ruben (HUMA-) HUMAN GENOME SCI INC Rosen CA, Barash SC,

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

AGCAGGACAGGTTTGAGTTTACCCAGCCTTCCTTGAGTCTTGAATCTCACAGGCCTGCT 780

721

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK876950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represent sequences used in the exemplification of the present invention.
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Disclosure; SEQ ID NO 36575; 3071pp + Sequence Listing; English.
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Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker for prostate cancer, is useful in gene therapy techniques to restore HPC2 normal levels by which neoplastic growth is suppressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; s: gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla; sequencing primer; PCR primer.
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                                                                                                                                                                                                                                                                             Human prostate cancer predisposing gene (HPC2) cDNA coding_sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 145.8; DB 24; Length 2481;
Pred. No. 8.4e-32;
1; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2481 BP; 588 A; 686 C; 711 G; 496 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding HPC2 paralogues and orthologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 128-131; 239pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOSP-) HOSPITAL FOR SICK CHILDREN.
                                                                                                                                                                        BP
                                                                  16215 CAGCGGAAGCTTTGACCGGAT 16195
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llarity 89.1%;
Conservative
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                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MYRI-) MYRIAD GENETICS
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P-PSDB; AAU73586.
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                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                               Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; antionvolusant; ostopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                            hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                   cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                             1605
                                                                                                                                                                                                                                                                                                                                                                                                       SCID; AIDS;
457
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                                                                                                                                                                                                                                                                                                                                                                        antianaemic; gene therapy; cancer; proliferative disorder; hyperter
neurodegenerative disorder; osteoarthritis; graft vs host disease;
cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; Al
398 TGTGGTGAGGGCACRTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGGTC
               1546 TGTGGTGAGGGCACATTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACCAGGTC
                                                                       1606 CTGGGCACCCTGGCTGCTGTTTGTGTCCCACCTGCACGAGATCACCACACGG 1660
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                                                           CTGGGCACCCTGGCTGTGTTTGTGTCCCACCTGCACGCAGGTCACCACACGG
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                                                                                                                                                                                                                                                      Human ORFX ORF2000 polynucleotide sequence SEQ ID NO:3999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 3179-3180; 5507pp; English.
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                                                                                                                                                                AAC76445 standard; cDNA; 2546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombosis; contraceptive; ss
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                            AAC76445;
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proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinfiammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; mouse; HPC2; prostate cancer; neoplastic growth; dytostatic; ss; gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla; sequencing primer; PCR primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1144 TGTGGTGAGGCACATTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGGTGAGGGCACRTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1204 CTGGGCACCCTGGCTGCTGTTTGTGTCCCCACCTGCAGCTGCAGATCACCACACGG 1258
                                                                                                                                                                                                                                                                                                                                                                                                 Score 145.8; DB 21; Length 2546;
Pred. No. 8.6e-32;
1; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    458 CTGGGCACCCTGGCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGG
                                                                                                                                                                                                                                                                                                                                        Sequence 2546 BP; 652 A; 643 C; 686 G; 564 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MYRI-) MYRIAD GENETICS INC. (HOSP-) HOSPITAL FOR SICK CHILDREN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS99133 standard; cDNA; 2892 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                18.2%;
89.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAY-2001; 2001WO-US14602.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tavtigian SV, Teng DHF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-066599/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gorilla ELAC2 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAU73593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gorilla gorilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200185911-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS99133;
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS99133
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gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in gene therapy techniques to suppress neoplastic growth of recipient cells which carry the mutant HPC2 allele. The sequences represent primers used in the methods of the invention, CDNA encoding human and mouse HPC2 and

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associated with cancer in a human. The method involves analysing an HPC2 gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in gene. Therapy techniques to suppress neoplastic growth of recipient cells which carry the mutant HPC2 allele. The sequences represent primers used in the methods of the invention, cDNA encoding human and mouse HPC2 and cDNA encoding human and mouse HPC2 and
                                                                                                                                                                                                                                                                                 1486 ATTCGAAATGTCAGTGCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGAC 1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; s:
gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla;
sequencing primer; PCR primer.
                                                                                                                                                                                                         338 AGTGGCAGTGACTCTTCTTCTTCTTCTGCAGCCCCGACACGTCTCTGCTACTGGAC 397
                                                                                                                                                                                                                                                                    TGTGGTGAGGGCACRTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid sequence encoding HPC2 polypeptide, which is marke for prostate cancer, is useful in gene therapy techniques to restore HPC2 normal levels by which neoplastic growth is suppressed in
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                         DB 24; Length 2892;
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                                                                                                                                                                                                                                                                                                                            CTGGGCACCCTGGCTGTGTTTGTGTCCCCACCTGCACGCAGATCACCACACGG
                                                                                                                                                  Score 145.8; DB 24; Length
Pred. No. 9.1e-32;
1; Mismatches 18; Indels
                                                                                                                      Sequence 2892 BP; 704 A; 787 C; 815 G; 586 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rommens JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MYRI-) MYRIAD GENETICS INC.
(HOSP-) HOSPITAL FOR SICK CHILDREN.
                                                                                                                                                                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                                                               AAS99132 standard; cDNA; 2908
                                                                                                                                                  18.2%;
89.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                Best_Local Similarity 89.1
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tavtigian SV, Teng DHF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimpanzee ELAC2 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-066599/09.
P-PSDB; AAU73592.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS99132;
                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                  398
                                                                                                                                                                                                                                                                                                                           458
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The invention relates to a human prostate cancer predisposing gene coding for an HPC2 polypeptide. The DNA and protein sequences are useful as diagnostic reagents for identifying a mutant HPC2 nucleotide sequence in a suspected mutant HPC2 allele by comparing the sequence of the suspected mutant HPC2 allele with a wild type HPC2 sequence. The sequences are also useful for detecting an alteration in HPC2, where the alteration is associated with cancer in a human. The method involves analysing an HPC2

Claim 87; Page 198-201; 239pp; English.

recipient cell

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                                                                                                                                                                                     338 AGTGGCAGTGACTCTTCTTCTTCTTCTTCTGCACCCCGACACGTCTCTGCTACTGGAC 397
                                                                                                                                                                                                                           TGTGGTGAGGGCACRTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGGTC 457
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                              Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies, useful for treatment and diagnosis of prostate cancer
                                                                                                                    Score 145.8; DB 24; Length 2908;
Pred. No. 9.1e-32;
L: Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e cancer predisposing gene; HPC2; chromosome 17p; peptide therapy; drug design; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate cancer predisposing gene HPC2 coding sequence.
                                                                                                                                                                                                                                                                                CTGGGCACCCTGGCTGCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACAGG
                                                                                          Sequence 2908 BP; 712 A; 788 C; 819 G; 589 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rommens JM;
                                                                 cDNA encoding HPC2 paralogues and orthologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 98-100; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tavtigian SV, Teng DHF, Simard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
51.2531
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "HPC2"
                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                          AAA58453 standard; cDNA; 2958
                                                                                                                     18.2%;
89.1%;
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/product= '
                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                Conservative
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                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-1998;
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                                                                                                                                              Matches 156;
                                                                                                                     Query Match
                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                        1606
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cDNA encoding HPC2 paralogues and orthologues.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; ss; gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla; sequencing primer; PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker for prostate cancer, is useful in gene therapy techniques to restore HPC2 normal levels by which neoplastic growth is suppressed in
                                                                                                                                                                                                                                                                                      1596 TGTGGTGAGGGCACATTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGGCAGGGTC 1655
                                                                                                                                                                                                      1536 ATTCGAAATGTCAGTGCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGAC 1595
                                                                                                                                                                                 338 AGTGGCAGTGACTCTTCTTCTTCTTCTGCAGCCCCGACACGTCTCTGCTACTGGAC 397
                                                                                                                                                                                                                                                                 457
                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                 TGTGGTGAGGGCACRTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC
cloning and sequencing the region of the genome which cause a predisposition to prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                     CTGGGCACCCTGGCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGG: 512
                                                                                                   DB 21; Length 2958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate cancer predisposing gene (HPC2) extended cDNA
                                                                                                                                           Indels
                                                           Sequence 2958 BP; 707 A; 805 C; 848 G; 598 T; 0 other;
                   to prostate cancer
                                                                                               Score 145.8; DB 21;
Pred. No. 9.2e-32;
1; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rommens JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MYRI-) MYRIAD GENETICS INC. (HOSP-) HOSPITAL FOR SICK CHILDREN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS98917 standard; cDNA; 2958 BP
                                                                                                 Query Match 18.2%;
Best Local Similarity 89.1%;
Matches 156; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-066599/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
  isolated by appeared to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAR-2002
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                                                                                                                                                                                                                                                               398
                                                                                                                                                                                                                                                                                                                                                458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                   1536 ATTCGAAATGTCAGTGCCACACTTGTCAACATAAGCCCCGACACGTCTCTGGTACTGGAC 1595
                                                                                                                                                                                                                        457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                338 AGTGGCAGTGACTCTCTTCCTCTTCTTCTGCAGCCCCGACACGTCTCTGCTACTGGAC 397
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto J;
                                                                                                                                                                                                                                                           1596 TGTGGTGAGGGCACATTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC
                                                                                                                                                                                                                        398 TGTGGTGAGGGCACRTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC
                                                                                                                                                                                                                                                                                                                 1656 CTGGGCACCCTGGCTGCTGTTTGTGTCCCACCTGCACGAGATCACCACACGG 1710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention describes primer sets for synthesising 5602
                                                                                                           ;
                                                                        DB 24; Length 2958;
                                                                                                                                                                                                                                                                                                458 CTGGGCACCCTGGCTGCTGTGTTTGTCCCACCTGCACGCAGATCACCACAGG
                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saito K, Yo
Otsuki T;
                                   Sequence 2958 BP; 707 A; 805 C; 848 G; 598 T; 0 other;
                                                                      18.2%; Score 145.8; DB 24;
89.1%; Pred. No. 9.2e-32;
11ve 1; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID 11557; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isogai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA sequence SEQ ID NO:11557
                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAH14250 standard; cDNA; 2976
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2000JP-0118776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUN-2001 (first entry)
                                                                                       Best Local Similarity 89.1
Matches 156; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1074617-A2.
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11-JAN-2000;
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Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH14250;
                                                                        Query Match
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             in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
neuroprotective; antiparkinsonian; protein therapy; EST;
                                                                                                                            oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTS). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat
 specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                          1676
                                                                                                                                                                                                                                                                                               TGTGGTGAGGGCACRTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC 457
                                                                                                                                                                                                                                                                           AGTGGCAGTGACTCTTCTTCTTCTTCTGCAGCCCCGACACGTCTCTGCTACTGGAC 397
                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                         1617 TGTGGTGAGGGCACATTTGGGCAGCTGTGCCGTCATTACGAGACACCAGGTGCACAGGGTC
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نتا
                                                                                                                                                                                                                                                                                                                                                                                                         CTGGGCACCCTGGCTGCTGTTTGTGTCCCACCTGCACGCAGATCACCACACGG 512
                                                                                                                                                                                                            Length 2976;
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                                                                                                                                                                                                                                            18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao QA,
                                                                                                                                                                             Sequence 2976 BP; 712 A; 807 C; 856 G; 601 T; 0 other;
                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang J,
RT;
                                                                                                                                                                                                          Score 145.8; DB 2.
Pred. No. 9.3e;32;
1; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human coding sequence SEQ ID NO: 240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 240; 509pp; English.
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r, Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed sequence tag; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN59829 standard; cDNA; 2992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhou P, As
Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-SEP-2001; 2001WO-US26015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-2000; 2000US-0659671.
                                                                                                                                                                                                              18.2%;
                                                                                                                                                                                                                               89.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                invention.
                                                                                                                                                                                                                                            Conservative
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P-PSDB; ABB97416.
                                                                                                                                                                                                                             Similarity
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                the present
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                                                                                                                                                                                                                                            Matches 156;
                                                                                                                               represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YT,
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                                                                                                                                                                                                                                                                                                                                        398
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multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a coding sequence of the
                                                                                                                                                                                                                                                                       1560 ATTCGAAATGTCAGTGCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGAC 1619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes human sulphatase G (hSG). hSG:is not a member of the well-characterised CTPSR sulphatase family. It belongs to a family showing sequence similarity to a sulphatase from the marine bacterium Alteromonas carrageenovora. The hSG gene contains 23 exons and is located at chromosome 17p11.2. The present sequence is clone lambda29.1 from a human testes CDNA library. It was
                                                                                                                                                                                                                                                       TGTGGTGAGGGCACRTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC 457
                                                                                                                                                                                              AGTGGCAGTGACTCTCTCTCTCTCTCTGCAGCCCCGACACGTCTCTGCTACTGGAC 397
                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                CTGGGCACCCTGGCTGCTGTTTGTGTGTCCCACCTGCACGCAGATCACCACACGG 512
                                                                                                                                    Score 145.8; DB 24; Length 2992;
Pred. No. 9.3e-32;
1; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human sulphatase G; hSG; chromosome 17p11.2; gene therapy; ss.
                                                                                                        Sequence 2992 BP; 725 A; 807 C; 859 G; 601 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encodes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated DNA sequence which enout useful in gene therapy for ase deficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Page 29-30; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "hSG"
                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                    AAA52810 standard; cDNA; 2478
                                                                                                                                     18.2%;
89.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human sulphatase G cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sulfatase deficiency
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                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAY99850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragment useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40200034327-A1.
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                                                                                                                                                                 156;
                                                                              invention.
                                                                                                                                     Query Match
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isolated using human EST sequences with sequence similarity to the non-CTPSR family as a probe to screen the library. The CDNA insert was subcloned and the DNA sequence of both strands was determined. The sequence may be used to treat a patient suffering from hSG deficiency by replacing, repairing, or compensating for a DNA sequence within that patient's genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1486 ATTCGAAATGTCAGTGCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGAC 1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 AGTGGCAGTGACTCTTCTTCTTCTTCTGCAGCCCCGACACGTCTCTGCTACTGGAC 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398 TGTGGTGAGGGCACRTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1606 CTGGGCACCCTGGCTACTGTGTTGTGTCCCACCTGCACGCAGATCACCACGGG.1660
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                                                                                                                                                                                                                                                                                                                                    DB 21; Length 2478;
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                                                                                                                                                                                                                                                                      Sequence 2478 BP; 587 A; 686 C; 709 G; 496 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                           Score 144.2; DB 2
Pred. No. 2.5e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 8011; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS72207 standard; cDNA; 1402 BP
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                                                                                                                                                                                                                                                                                                                                           18.0%;
88.6%;
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                            Matches 155; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                           Query Match
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a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; ds;
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                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human prostate cancer predisposing gene (HPC2) DNA partial exon #17.
                                                                                                                                                                                                                                                                                                                                                    674 AGCCCCGACACCTCTCTACTACTGGACTGTGGTGAGGGCACATTTGGGCAGCTGTGCCGT
                                                                                                                                                                                                                                                                                                                            371 AGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACRTTTGGGCAGCTGTGCCGT
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                                                                                                                                                                                                                                                                 DB 23; Length 1402;
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                                                                                                                                                                                                                               Sequence 1402 BP; 338 A; 371 C; 377 G; 316 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate cancer predisposing gene.
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                                                                                                                                                                                                                                                                                 .le-30;
                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                               Score 141.6;
Pred. No. 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HOSP-) HOSPITAL FOR SICK CHILDREN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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99.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAY-2000; 2000US-0564805
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                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy;
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                                                                                                                                                                                                                                                                                                 141;
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                                                                                                                                                                                                                                                                 Query Match
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 The sequences are also
               useful for detecting an alteration in HPC2, where the alteration is associated with cancer in a human. The method involves analysing an HPC2 gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in gene therapy techniques to suppress neoplastic growth of recipient cells which carry the mutant HPC2 allele. The sequences represent DNA encoding human and mouse HPC2 and fragments of HPC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker for prostate cancer, is useful in gene therapy techniques to restore HPC2 normal levels by which neoplastic growth is suppressed in
                                                                                                                                                                                                                                                                                                                                             CCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACRTTTGGGCAGCTGTGCCGTCA 432
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                                                                                                                                                                                          Length 139;
                                                                                                                                                                                      Score 138.6; DB 24; Length
Pred. No. 2.4e-30;
1; Mismatches 0; Indels
mutant HPC2 allele with a wild-type HPC2 sequence.
                                                                                                                                                      Sequence 139 BP; 23 A; 43 C; 43 G; 30 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MYRI-) MYRIAD GENETICS INC.
(HOSP-) HOSPITAL FOR SICK CHILDREN.
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99.3%;
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Matches 138; Conservative
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P-PSDB; AAU73591.
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                gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in gene therapy techniques to suppress neoplastic growth of recipient cells which carry the mutant HPC2 allele. The sequences represent primers used in the methods of the invention, cDNA encoding human and mouse HPC2 and cDNA encoding HPC2 paralogues and orthologues.
associated with cancer in a human. The method involves analysing an HPC?
                                                                                                                                                                                                                                                                                                                                                                                                                                 1451 GAAATGTCAGTTCCACACTCGTCAACCTAAGCCCTGACAAGTCAGTGCTCCTGGATTGTG 1510
                                                                                                                                                                                                                                                                                                                  342 GCAGTGACTCTTCTTCTTTCTCTTCTGCAGCCCCGACGTCTCTGCTACTGGACTGTG 401
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                                                                                                                                                                                                                                                                          43;
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Pred. No. 4.2e-19;
0; Mismatches 43,
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Job time: 263.416 secs
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Human nervous syst

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Human immune/haema Human cDNA clone (Human cDNA sequenc

Title: Perfect score:

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Human; prostate cancer predisposing gene; HPC2; chromosome 17p; gene therapy; peptide therapy; drug design; ds.
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/product= "HPC2"
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Copyright (c) 1993 - 2003 Compugen Ltd.
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The present sequence is the genomic sequence of the human prostate cancer predisposing gene HPC2, which is found on chromosome 17p. Some alleles of this gene cause a predisposition to cancer, particularly prostate cancer. This gene and its protein can be used in peptide and gene therapy for cancer patients, as well as being useful as diagnostic clools (both for cancer sufferers and those with a predisposition to the disease) and in the production of cancer drugs. This sequence was isolated by cloning and sequencing the region of the genome which appeared to cause a predisposition to prostate cancer.
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                                                                                   Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies, useful for treatment and diagnosis of prostate cancer
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100.0%; Pred. No. 3.3e-125;
tive 0; Mismatches 0;
              Rommens JM;
                                                                                                                             Claim 3; Page 108-122; 157pp; English.
              Simard J,
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                                                                                                                                                                                                                                                                                                                        The invention relates to a human prostate cancer predisposing gene coding for an HPC2 polypeptide. The DNA and protein sequences are useful as diagnostic reagents for identifying a mutent HPC2 nucleotide sequence in a suspected mutent HPC2 allele by comparing the sequence of the suspected mutent HPC2 allele with a wild-type HPC2 sequence. The sequences are also useful for detecting an alteration in HPC2, where the alteration is sosciated with cancer in a human. The method.involves analysing an HPC2 gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in gene therapy techniques to suppress neoplastic growth of recipient cells which carry the mutant HPC2 allele. The sequences represent DNA encoding human and mouse HPC2 and fragments of HPC2.
           HPC2; prostate cancer; neoplastic growth; cytostatic; ds;
prostate cancer predisposing gene.
                                                                                                                                                                                                                                             Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTACACATAAGAAAGCTGAGGCTCTGAGAGGTCAAGATCACGCAGCTAACAAATGAGCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                       for prostate cancer, is useful in gene therapy techniques to restore HPC2 normal levels by which neoplastic growth is suppressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TATCAGGTGACTGAATTCTATATTCTGAAGTAGGAGATACTGTTATTGCTGTTATTACAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATCAGGTGACTGAATTCTATATTCTGAAGTAGGAGATACTGTTATTGCTGTTATTACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACGTAAAAATGATCAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITITGITITGITITGITITGITITGAGACAGGGTCTCGAGGTGTCACCCAGGCTGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTCCGCGCTTAAGCGATTCTCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTTCGCGCGTTAAGCGATTCTCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 26664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26664 BP; 6173 A; 6300 C; 6519 G; 7661 T; 11 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 500; DB 24;
; Pred. No. 3.3e-125;
0; Mismatches 0;
                                                                                                                                                                                                 Rommens JM;
                                                                                                                                                                                                                                                                                                   Claim 3; Page 143-157; 239pp; English.
                                                                                                                                                                                                 Simard J,
                                                                                                                                                              (MYRI-) MYRIAD GENETICS INC.
(HOSP-) HOSPITAL FOR SICK CHILDREN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
100.0%;
                                                                                                                07-MAY-2001; 2001WO-US14602.
                                                                                                                                        05-MAY-2000; 2000US-0564805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               500; Conservative
                                                                                                                                                                                               Tavtigian SV, Teng DHF,
                                                                                                                                                                                                                      WPI; 2002-066599/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                  WO200185911-A2.
                                                                                                                                                                                                                                                                                recipient cell
                      gene therapy;
                                             Homo sapiens
                                                                                         15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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Matches
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This is the 14-3-3 sigma transcriptional regulatory region nucleotide sequence. 14-3-3 sigma is a member of the 14-3-3 protein family and is also known as HMEI or stratifin. 14-3-3 sigma expression is regulated by p53 and exogenous expression of 14-3-3 sigma expression is regulated by p53 and exogenous expression of 14-3-3 sigma results in G2 block. The 14-3-3 sigma nucleotide and amino acid sequences are used in the invention to develop agents for the diagnosis, susceptibility.

Invention to develop agents for the diagnosis, susceptibility to a method for suppressing the growth of tumour cells. The 14-3-3 sigma probes can be used for diagnosing, testing susceptibility to or treating cancers and identifying agents for treating cancers. They can also be used to treat other proliferative diseases, ceg. psoriasis, polyps, warts, and inflammatory diseases. The 14-3-3 sigma antisense oligonucleotides can be used for promoting the proliferation and growth of cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-3-3 sigma; HMEL; stratifin; p53; diagnosis; cancer; psoriasis; polyp; psoriasis; wart; inflammatory disease; proliferation; ss; transcription regulatory region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of 14\text{-}3\text{-}3 sigma polypeptides and nucleic acids for the diagnosis or treatment of cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                       14-3-3 sigma transcription regulatory region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 52; Page 68-71; 73pp; English.
                                                                                                                                                                                                       BP.
                                                                                                                                                                                                   AAX89439 standard; DNA; 7680
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98US-0210748.
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AAGCTCTGAGGGACTGACGT
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2000US-0231244
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      05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
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08-SEP-2000;
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12-SEP-2000;
14-SEP-2000;
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21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
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13-0CT-2000
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17-NOV-2000;
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01-NOV-2000;
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14-SEP-2000
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27-SEP-2000
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 184 TIGITITIGITITIGITITIGITITIGAGACAGGGICCICGAGGIGICACCAGGCIGGAGIGCA 243
                                                                                                                                                                                          Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21382
        6006 GIGGCGCCATCTCGCTCACTGCAACGTCCGCCTCCCGGGTTCAAGCGATTCTCCTGCCT
                                244 GIGGCGCGATITCGACTCACCGCAACCICCGCCT-CCGCGCTTAAGCGATICICCTGCCT
                                                                AAK66570 standard; DNA; 10708 BP
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2000US-0184664
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                                                                                                                                                         06-NOV-2001 (first entry)
                                                                                                                                                                                                                                  WO200157182-A2
                                                                                                                                                                                                                   Homo sapiens.
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RESULT 5
                                                                                                                  AAK54951 to Ak64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
c supplement the patients own production of (I). Additionally, (I)
c protein. (I) proteins and polynucleotides may be used to prevent,
c protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic-derived cells. ARK64703
cto AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK87650 and AAM82169
crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTITIGITITGITITGITITGITITGAGACAGGGICTCGAGGTGTCACCCAGGCTGGAG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 TGCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTCCGCGCTTAAGCGATTCTCCTG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 10708;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10708 BP; 2285 A; 3103 C; 3106 G; 2214 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 120.2; DB 2
Pred. No. 1.9e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM
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83.0%;
                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                    000US-0251856
                                                                                                                                                                                                                                                                                                                                    000US-0251990
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                                                                                                                                                                                 000US-0250391
                                                                                                                                                                                                                                                                                                                                                     000US-0254097
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-483426/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                 7-NOV-2000;
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                                                                 7-NOV-2000;
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This sequence represents the human neuregulin-1 associated gene 1 (NRG1AG1) of the invention. The NRG1AG1 gene is also referred to as the human Schizophrenia gene. The invention also relates to fragments or variants of the gene and the NRG1AG1 polypeptides they encode. The NRG1AG1 nucleic acids and polypeptides may be used in the prevention diagnosis and treatment of diseases associated with inappropriate NRG1AG1 expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of NRG1AG1 by expressing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               patients may be in need of restorative therapy. The NRGIAGI polypeptides may also be used as afrigens in the production of antibodies against NRGIAGI and in assays to identify modulators of NRGIAGI expression and activity. Anti-NRGIAGI antibodies and antagonists may also be used to down regulate expression and activity. Anti-NRGIAGI antibodies may also be used as diagnostic agents for detecting the presence of NRGIAGI polypeptides in samples. NRGIAGI Is associated with schizophrenia which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1503900 BP; 452487 A; 281874 C; 288074 G; 480092 T; 1373 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuregulin-1 associated gene 1 nucleic acids and fragments, useful for preventing diagnosing and treating schizophrenia \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 CAAAAAACACTACAATTTTTGTTTTGTTTTGTTTTGAGACAGGGTCTCGAGGTGT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAG67900, AAG67901, AAG67902, AAG67903, AAG67904, AAG67905, AAG67906, AAG67907, AAG67908, AAG67909, AAG67910, AAG67911, AAG67912, AAG67913, AAG67914, AAG67915, AAG67916, AAG67917, AAG67918, AAG67919, AAG67920, AAG67921, AAG67922, AAG67922, AAG67922, AAG67923, AAG67924, AAG67928, AAG67928, AAG67933, AAG67931, AAG67938, AAG67931, AAG67933, AAG67931,
                                                                                                                                                                                                                                                                                                                                                                 neuregulin-1 associated gene 1; NRGIAG1; Schizophrenia gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    may be prevented, diagnosed and/or treated by the above methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 120; DB 22;
Pred. No. 1.1e-21;
0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gulcher JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 90-501; 750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steinthorsdottir V,
AAK95240 standard; DNA; 1503900 BP.
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82.8%;
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                                                                                                                                                                            17-DEC-2001 (first entry)
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Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-550179/61
                                                                                                                                                                                                                                                                           Human neuregulin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200164876-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stefansson H,
                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2000;
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                                                                                      AAK95240;
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                                                                                                                                                                                                                                                  Sequence 1503900 BP; 452487 A; 281874 C; 288074 G; 480092 T; 1373 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence represents the human neuregulin 1 gene of the invention
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                                                                                                                                        532425 CGCCCAGGCTGGAGTGCCAGGCGGGATCTCGGCTCACTGCAAGCTCCGCCTCCGGGGTT
                                                                                                                                                                                                              - AAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACG
                                                                         CACCCAGGCTGGAGTGCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTCCGCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuregulin 1 nucleic acids and proteins useful for diagnosing preventing and treating schizophrenia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGG7956, AAGG7957, AAGG7958, AAGG7959, AAGG7961, AAGG7961, AAGG7962, AAGG7963, AAGG7964, AAGG7966, AAGG7969, AAGG7969, AAGG7969, AAGG7969, AAGG7969, AAGG7969, AAGG7969, AAGG7969, AAGG7969, AAGG79712, AAGG79712, AAGG79712,
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AAG67950, AAG67951, AAG67952, AAG67953, AAG67954, AAG67955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; neuregulin 1 gene; schizophrenia; gene therapy; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAG67938, AAG67939, AAG67940, AAG67941,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK96733 standard; DNA; 1503900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human neuregulin-1 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Human; reproductive system related antigen; reproductive system disorder;
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                                                                           166 CAAAAAACACTACAATTTTTGTTTTGTTTTGTTTTGAGACAGGGTCTCGAGGTGT 225
                                         Gaps
                                                                                                  532425 CGCCCAGGCTGGAGTGCACTGGGGGATCTCGGCTCACTGCAAGCTCCGCCTCCGGGGTT
                                                                                                                                                      226 CACCCAGGCTGGAGTGCAGTGGCGCGATTTCGACTCACCGCAACCTCGGCCTCCGCGCTT
                                                                                                                                                                                                                               286 -AAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human reproductive system related antigen DNA SEQ ID NO: 8718
                                       Indels
                                                                                                30;
 ; DB 22;
1.1e-21;
                                       0; Mismatches
                     Pred. No.
24.0%;
82.8%;
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                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; gene therapy; ds
                   Best Local Similarity
Matches 149; Conser
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05-SEP-2000;
05-SEP-2000;
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06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTGTTTTGTTTTGAGACAGGGTCTCGAGGTGTCACCCAGGCTGGAGTGCAGTGGCGGG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTCGACTCACCGCAACCTCCGCCTCCGCGCTTAAGCGATTCTCCTGCCTCAGCCTCCCA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 133 TTAGAGCTTGTCCTCTATTCTTGCTTTTCCAAAAAACACTACAATTTTTGT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.0%; Score 119.8; DB 22; Length 4045; llarity 73.0%; Pred. No. 1.8e-22; Conservative 0; Mismatches 57; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 8718; 1297pp + Sequence Listing; English.
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                   2000US-0249245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME
                                                                                                                                                                   -S00003
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Matches 154; Conserv
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05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
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.7 - NOV - 2000;
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08-DEC-2000;
                   17 - NOV - 2000;
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ID AAL0
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AAL06031 standard; DNA; 4045 BP

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08-NOV-2000
                                                                                                             Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                                      Human reproductive system related antigen DNA SEQ ID NO: 8719.
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21-NOV-2001 (first entry)
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20000S-023703
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28-JUN-2000;
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L-JUL-2000;
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                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         testicular antigen; testes; cancer; metastasis; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1603 TICTACATIGGCITCTITCTCGTTCCTTCCTTCCTTCCTTCTTCTTCTTCTCTCT 1662
                                                                                                                                                                                                 Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition \cdot
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                                                                                                                                                                                                                                                                                                                                                                                                                             133 TTAGAGCTTGTCCTCTATTCTTGCTTTTCCAAAAAACACTACAATTTTTGTTTTGT 192
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                                                                                                                                               Ruben SM
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20000S-0251990.
20000S-0254097.
20010S-0259678.
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2000US-0251869
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Best Local Similarity
Matches 154; Conserv
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                        08-DEC-2000;
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           The present invention provides the protein and coding sequences of 973 muman testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a protein fragment of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder;
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                                                                                                                                                                                                                                                        1723 TCTCAGCTCACTGCAACCTCTGCCTCTGAGTTCAAGCGATTCTCCTGCCTCAGCCTCCCA 1782
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                                                                                                                                                                                              Gaps
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                                                                                                                                                                   Length 4045;
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                                                                                                                                    Sequence 4045 BP; 1044 A; 994 C; 1001 G; 1006 T; 0 other;
                                                                                                                                                               Score 119.8; DB 23; Length
Pred. No. 1.8e-22;
0; Mismatches 57; Indels
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                                                                                                                                                                              Best Local Similarity 73.0%;
Matches 154; Conservative
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26-JUL-2000;
26-JUL-2000;
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24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 3247; 766pp; English.
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He H 14-MC-2000; 200008; 0225213.

RE 11-MC-2000; 200008; 0225213.

RE 11-MC-2000; 200008; 0225213.

RE 11-MC-2000; 200008; 0225214.

RE 12-MC-2000; 200008; 0225214.

RE 22-MC-2000; 200008; 0225214.

RE 23-MC-2000; 200008; 0225214.
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The present invention provides the protein and coding sequences of 973 muman testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and assatrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a protein fragment of the invention.
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2000US-0246524
2000US-0246525
2000US-0246525
2000US-0246526
2000US-0246528
2000US-0246532
2000US-0246610
2000US-0246611
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Best Local Similarity 73.0%;
Matches 154; Conservative (
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133 TTAGAGCTTGTCCTCTATTCTTGCTTTTCTTTCCAAAAAACACTACAATTTTTGTTTTGT 192

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GCGCTTAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACA
              220 AGGTGTCACCCAGGCTGGAGTGCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTCC
                                                                                                                                                                                                                                                                                                             RANTES; T-cell; T-lymphocyte; heparanase; heparin
arthritis; restenosis; cancer; wound healing; ss.
                                                                                                                                                                                                        AAQ85372 standard; cDNA; 1160
                                                                                                                                          12521 TGACGCCTAGCTAAT 12507
                                                                                                                  340 CCACGTAAAAATGAT
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                                                                                        1723 TCTCAGCTCACTGCAACCTCTGCCTCTGAGTTCAAGCGATTCTCCTGCCTCAGCCTCCCA 1782
                                     of disrupted in schizophrenia 1 (DIS1) introm 8.
                         193 TTTGTTTTGTTTTGAGACAGGGTCTCGAGGTGTCACCCCAGGCTGGAGTGCAGTGGCGCGA
                                                                           253 TTTCGACTCACCGCAACCTCCGCCTTCGCGCTTAAGGGGATTCTCCTGCCTCAGCCTCCCA
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75.9%; Pred. No. 3.6e-22;
.ive 0; Mismatches 47; Indels 0;
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psychiatric disorder; ss.
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(MEDI-) MEDICAL RES COU
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93US-0099866. 93US-0136117. 94WO-US08207

heparin; heparan sulfate;

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(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATTTTTGTTTTGTTTTGTTTTGTTTTTGAGACAGGGTCTCGAGGTGTCACCCCAGGCTGGA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         767 ATTTTTTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTCTGTCGCCCAGGCTGGA 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTTCCGCGCTTAAGCGATTCTCCT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                 Purified heparanases, prepared under reducing conditions and activated with transglutaminase, are given in AAR70786-805. Most are prepared by reverse transcription of mRNA from activated human leukocytes, then cloning of the cDNA into pvL1392 baculovirus vector, and expression in Sf9 cells in the presence of reduced glutathione and dithiothreitol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detecting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 1160;
                                                                                                                                                                           cancer.
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Pred. No. 1.3e-22;
0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 GCCTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACG 344
                                                                                                                     Screening for cpds. with anti-heparanase activity - by inhibition of heparin or heparan sulphate degradation, potentially useful for treating arthritis, restenosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1160 BP; 298 A; 332 C; 295 G; 235 T; 0 other;
                                                                                                                                                                                                                          Disclosure; Page 51-52; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.9%;
82.5%;
SR;
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Ledbetter
                                         WPI; 1995-082239/11.
P-PSDB; AAR70802.
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Matches 137; Conserv
Hoogwerf AJ,
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Gaps

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Best Local Similarity 75.9 Matches 148; Conservative

AAF21050 standard; DNA; 1160 BP.

RESULT 14 AAF21050/c

AAF21050;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGCAGTGGCGCGATCTCGGCTCACTGCAAGCTCCGCTCCCGGGTTCACGCCATTCTCCT 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 AATTITIGITTIGITTIGITTIGITTIGITTIGAGACAGGGICTCGAGGIGICACCCAGGCIGGA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Using chemokine antagonists for treating or preventing viral infection - particularly by human immunodeficiency virus, also new polypeptide antagonists derived from RANTES and related nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bachelerie F, Baggiolini M, Virelizier JL, Arenzana-Seisdedos F;
Clark-Lewis I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTTCGCGCGTTAAGCGATTCTCCT
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Pred. No. 1.3e-22;
0; Mismatches 29; Indels 0;
GCCTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1160 BP; 298 A; 332 C; 295 G; 235 T; 0 other;
                                                                                                                                                                                                              Chemokine; RANTES; antagonist; antiviral; HIV; ds.
                                                                                                                                                                                cDNA containing the sequence coding for RANTES.
                                                                                                                                                                                                                                                                  Location/Qualifiers
96..302
                                                                                                                                                                                                                                                                                                          /*tag= a
/product= RANTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1A; 41pp; French.
                                                                                        AAV36275 standard; DNA; 1160 BP
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Best Local Similarity 82.5%;
Matches 137; Conservative
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                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                   01-SEP-1998
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                                                                                                                   AAV36275;
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oligonuclectides and compositions (1) comprising them. In the antisense oligonuclectides the A is replaced by a 'Universal' or alternative base. (7) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonuclectides and (1) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and mallignancies, such as stimulating and antipodies and mallignancies, such as stimulating and changing and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide

The present invention describes low adenosine (A) content antisense

Page 856-857; 1592pp; English.

Disclosure;

transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasconostriction, inflammation, allergy(ies) allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR).

(RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypetrension, emphyseam, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide

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Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                      Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -
                                          Human low adenosine antisense oligonucleotide related sequence #2617.
                                                                                                                                                                                                                                                              24-MAR-2000; 2000WO-US08020.
                                                                                                                                                                                                                                                                                                           EAST CAROLINA
                     (first entry)
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                                                                                                                                                                                             Homo sapiens.
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(NYCE/) NYCE
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                     14-MAR-2001
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                                                                                                                                                                     cancer; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis; monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV; MIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia; basophil-mediated disease; myocardial infarction; acute ischaemia; rheumatoid arthritis; contraception; ds.
fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention concerns the identification of a number of chemckines which can be used to produce derivatives, agonists and antagonists which are then useful in disease treatment. The chemckines include sequences AAB15785-B15794, AAB15803-B15813 and AAB1581-B15848.
                                                                                                                                                                                                     179 AATTTTTGTTTTGTTTTGTTTTGAGACAGGGTCTCGAGGGTGTCACCCAGGCTGGA 238
                                                                                                                                            239 GTGCAGTGCCCGATTTCGACTCACCGCAACCTCCGCCTCCGCGCTTAAGCGATTCTCCT 298
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide 3, amide and heterocyclic compounds and saccharide conjugates used for inhibiting chemokine induced activity and for treating e.g. stroke, vascular diseases, autoimmune diseases and t
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                                                                      DB 21; Length 1160;
                                                                   Score 119.6; DB 21; Length
Pred. No. 1.3e-22;
0; Mismatches 29; Indels
                                                                                                                                                                                                                                            299 GCCTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACG 344
                                                                                                                                                                                                                                                             Sequence 1160 BP; 298 A; 332 C; 295 G; 235 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human chemokine coding sequence SEQ ID NO: 78.
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/*tag= a
/product= "human chemokine"
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                                                                      23.9%;
82.5%;
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99US-0271192.
99US-0452406.
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                                                                                   Best Local Similarity 82.5
Matches 137; Conservative
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                the present invention.
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P-PSDB; AAB15790.
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01-DEC-1999;
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              autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated diseases, endotoxacemia, myocardial infarction, acute ischaemia and rheumatoid arthritis, and can be used to prevent strokes and as contraceptives. The chemokine coding sequences AAA74868-A74888 can be used in gene therapy for the same diseases, as well as in the production
                                                                                                                                                                                                                                                           179 AATTTTTGTTTTGTTTTGTTTTTGAGACAGGGGTCTCGAGGTGTCACCCAGGCTGGA 238
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                             GTGCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTCCGCGCTTAAGCGATTCTCCT
chemokine derivatives can be used to treat diseases such as
                                                                                                                                                                                      DB 21; Length 1160;
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                                                                                                                                                       Sequence 1160 BP; 298 A; 332 C; 295 G; 235 T; 0 other;
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Pred. No. 1.3e-
0; Mismatches
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Sequence:

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Human; prostate cancer predisposing gene; HPC2; chromosome 17p; gene therapy; peptide therapy; drug design; ds.
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ABQ69245
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AAH16379
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Novel human coding
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Human prostate can
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Copyright (c) 1993 - 2003 Compugen Ltd.
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The present sequence is the genomic sequence of the human prostate cancer predisposing gene HPC2, which is found on chromosome 17p. Some alleles of this gene cause a predisposition to cancer, particularly prostate cancer. This gene and its protein can be used in peptide and gene therapy for cancer patients, as well as being useful as diagnostic tools (both for cancer sufferers and those with a predisposition to the disease) and in the production of cancer drugs. This sequence was isolated by cloning and sequencing the region of the genome which appeared to cause a predisposition to prostate cancer.
                                                              Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies, useful for treatment and diagnosis of prostate cancer
           Simard J, Rommens JM;
                                                                                               Claim 3; Page 108-122; 157pp; English.
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           Teng DHF,
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          Tavtigian SV,
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                                   Length 26664;
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Sequence 26664 BP; 6173 A; 6300 C; 6519 G; 7661 T; 11 other;
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                                                                        Indels
                                   100.0%; Score 501; DB 21;
100.0%; Pred. No. 6.5e-157;
:ive 0; Mismatches 0;
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26524 ACCTIGGAGAAGGCTCTCTGTGCTGTAGTGTGGCAGCTGCCTGGTACCCGGGTGGCTTGG 26583
                                  AAGAAGTCAGCTCCCGTCGTAGTGAGCACCTCTGGAACCTGTCCTCAGAGGAGCCACCCTT 480
                                                                                                                                                                                                                                                                                                                 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36575
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               Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; gene therapy; prostate cancer predisposing gene.
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HPC2 normal levels by which neoplastic growth is suppressed in
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Pred. No. 6.5e-157;
Mismatches 0;
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                                                                                                                                                                                                                                                                                Rommens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human and mouse HPC2 and fragments of HPC2
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 143-157; 239pp; English.
                                                                                                                                                                                                                                                                                Simard J,
                                                                                                                                                                                                                            (MYRI-) MYRIAD GENETICS INC. (HOSP-) HOSPITAL FOR SICK CHILDREN
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Best Local Similarity 100.0%;
Matches 501; Conservative 0;
                                                                                                                                                              37-MAY-2001; 2001WO-US14602
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                                                                                                                                                                                                                                                                                                                                                                                              recipient cell
                                                               Homo sapiens
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PR 05-SEP-20000 2000US-0229513
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PR 08-SEP-20000 2000US-0231442
PR 08-SEP-20000 2000US-0231443
PR 08-SEP-20000 2000US-0231444
PR 08-SEP-20000 2000US-0231444
PR 12-SEP-20000 2000US-0231344
PR 14-SEP-20000 2000US-0231344
PR 14-SEP-20000 2000US-0231344
PR 14-SEP-20000 2000US-0231348
PR 14-SEP-20000 2000US-0231348
PR 14-SEP-20000 2000US-0231348
PR 14-SEP-20000 2000US-0231344
PR 25-SEP-20000 2000US-0231441
PR 25-SEP-20000 2000US-0234414
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (1)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (1) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
cappelement the patients own production of (1). Additionally, (1)

polynucleotides may be used to produce the secreted (1), by inserting
the nucleic acids into a host cell and culturing the cell to express the
polynucleotides may be used to produce the secreted (1), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (1) proteins and polynucleotides may be used to prevent,
clagnose and treat immune/haematopoletic-derived cells. AAK64703

concers and cancer metastases of haematopoletic antigen genomic
sequences from the present invention. AAK84942 to AAK84950 and AAM82169
crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12511 ACTAATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGCCACTTTC.12452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 501; DB 22; Length 37959; 100.0%; Pred. No. 7.9e-157; ive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
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05-JAN-2001; 2001US-0259678
2000US-0249217
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Best Local Similarity 100.0
Matches 501; Conservative
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08-DEC-2000;
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Sequence 655 BP; 165 A; 169 C; 199 G; 122 T; 0 other;
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nes 303;
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                                              Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a human prostate cancer predisposing gene coding for an HPC2 polypeptide. The DNA and protein sequences are useful as diagnostic reagents for identifying a mutent HPC2 nucleotide sequence in a suspected mutant HPC2 allele by comparing the sequence of the suspected mutant HPC2 allele with a wild-type HPC2 sequence. The sequences are also useful for detecting an alteration in HPC2, where the alteration is associated with cancer in a human. The method involves analysing an HPC2 gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in gene therapy techniques to suppress neoplastic growth of recipient cells which carry the mutant HPC2 allele. The sequences represent DNA encoding human and mouse HPC2 and fragments of HPC2.
                                                               CTCTAATCCAGCAAAGTGATTCCCTGCACACAGAGACAAGCAGAGTAACAGGATCAGTG 12392
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                                                                                                                          360
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                                          GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG
                                                                                                                        CAATTGTGAGTTCTTTTGCTTCCTCCTGCTGCTACAGAGCAGGGTCTGCTGTGCACC
                                                                                                                                                                                                      ACCTTGGAGAAGGCTCTCTGTGCTGTAGTGTGGCAGCTGCCTGGTACCCGGGTGGCTTGG
                                                                                                                                                                                                                                                                                      AAGAAGTCAGCTCCCGTCGTAGTGAGCACCTCTGGAACCTGTCCTCAGAGACCACCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MYRI-) MYRIAD GENETICS INC. (HOSP-) HOSPITAL FOR SICK CHILDREN.
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                                                                 ACTAATTTCATTTCAAGGCAGTTTTTTAAAGAAGTCTTGGAAACAGACGGCGCCCTTTC 180
                                 Gaps
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                                                                                                                                                               CTCTAATCCAGCAAAGTGATTCCCTGCACACCAGAGACAAGCAGAGTAACAGGATCAGTG
                                                                                                                                                                                                              GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG
                                                        GGTATGGAGCTGTGCCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies, useful for treatment and diagnosis of prostate cancer \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; prostate cancer predisposing gene; HPC2; chromosome 17p; gene therapy; peptide therapy; drug design; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate cancer predisposing gene HPC2 coding sequence
                                Indels
       Score 303; DB 24;
Pred. No. 3.2e-91;
0; Mismatches 0;
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51..2531
60.5%; Scor.
100.0%; Pre
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/product= "HPC2"
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                                Conservative
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alleles of this gene cause a predisposition to cancer, particularly prostate cancer. This gene and its protein can be used in peptide and gene therapy for cancer patients, as well as being useful as diagnostic tools (both for cancer sufferers and those with a predisposition to the disease) and in the production of cancer drugs. This sequence was isolated by cloning and sequencing the region of the genome which appeared to cause a predisposition to prostate cancer.
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                                                                                                                                                                                                                                                          Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; s:
gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla;
sequencing primer; PCR primer.
                                                                                                                                                                           Gaps
                                                                                                                                                                                                     1 GGTATGGAGCTGTGCCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT 60
                                                                                                                                                                                                                   2656 GGTATGGAGCTGTGCCGAGGCTTCCCACATAAGCACTAGTCTATAGATGCTTTT
                                                                                                                                                                                                                                                                                                                                GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG
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0
                                                                                                                                            60.5%; Score 303; DB 21; Length 2958; 100.0%; Pred. No. 7.4e-91; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate cancer predisposing gene (HPC2) extended cDNA.
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                                                                                                                   Sequence 2958 BP; 707 A; 805 C; 848 G; 598 T; 0 other;
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The invention relates to a human prostate cancer predisposing gene coding for an HPC2 polypeptide. The DNA and protein sequences are useful as diagnostic reagents for identifying a mutant HPC2 nucleotide sequence in a suspected mutant HPC2 allele by comparing the sequence of the suspected mutant HPC2 allele with a wild type HPC2 sequence. The sequences are also useful for detecting an alteration in HPC2, where the alteration is associated with cancer in a human. The method involves analysing an HPC2 gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in gene therapy techniques to suppress neoplastic growth of recipient cells which carry the mutant HPC2 allele. The sequences represent primers used in the methods of the invention, cDNA encoding human and mouse HPC2 and cDNA encoding HPC2 paralogues and orthologues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidialeatic; antidiabetic; antidiantantiant, antibacterial; antifungal; antitheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; proliferative disorder; hypertension; neurodegenerative disorder; soteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2836 CTCTAATCCAGCAAAGTGATTCCCTGCACAGAGACAAGCAGAGTAACAGGATGATG
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HPC2 normal levels by which neoplastic growth is suppressed in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2958 BP; 707 A; 805 C; 848 G; 598 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 303; DB 24;
Pred. No. 7.4e-91;
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                                                                 3; Page 134-136; 239pp; English.
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                        recipient cell
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                                                                    Claim
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The invention relates to a human prostate cancer predisposing gene coding for an HPC2 polypeptide. The DNA and protein sequences are useful as diagnostic reagents for identifying a mutant HPC2 nucleotide sequence in a suspected mutant HPC2 allele by comparing the sequence of the suspected mutant HPC2 allele by comparing the sequence of the suspected museful for detecting an alteration in HPC2, where the alteration is associated with cancer in a human. The method involves analysing an HPC2 gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in gene therapy techniques to suppress neoplastic growth of recipient cells gene the new parts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which carry the mutant HPC2 allele. The sequences represent primers used in the methods of the invention, cDNA encoding human and mouse HPC2 and
                                                                                                                                                                                                                                                                                                                                   Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; ss; gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla; sequencing primer; PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al nucleic acid sequence encoding HPC2 polypeptide, which is marker prostate cancer, is useful in gene therapy techniques to restore? Normal levels by which neoplastic growth is suppressed in
 2445 GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAGAGTTTG 2504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2606 GGTATGGAGCTGTGCCAAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT 2665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rommens JM;
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Pred. No. 1e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HOSP-) HOSPITAL FOR SICK CHILDREN.
                                                                                                                                                                                       AAS99132 standard; cDNA; 2908 BP.
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98.7%;
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                                                                                                                                                                                                                                                                 (first entry)
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CAA 2507
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                                                          CAA 303
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which represent the human ORRY open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipornal antipornal nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardlovascular disease, diabetes mellitus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nypertension, hypothyroidism, cholesterol ester storage, systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to AAB43397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erythematosus, severe combined immunodeficiency (SCID), AIDS, Viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
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Pred. No. 8.1e-90;
0; Mismatches 2;
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 thrombosis; contraceptive; ss
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99.3%;
                                                                                                                                                  2000WO-US08621.
                                                                                                                                                                                   31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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301; Conservative
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                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP
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                                                                        WO200058473-A2.
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Best Local S
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antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
neuroprotective; antiparkinsonian; protein therapy; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopolesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat
                                                                                                       2845
  2725
                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ited polynucleotide for treating diseases associated with its polypeptide such as cancer and multiple sclerosis -
2666 AGGACTGGTGCCTGGCACAGCCGGGGACAGGAGGCTGCCACACGGAAGCAAGGAGATGA
                                       GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG
                                                                                                                                             2846 GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG
                         ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCACCTTTC
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تا
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           725 A; 807 C; 859 G; 601 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Asundi V, Zhang J,
I, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                      Novel human coding sequence SEQ ID NO: 240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 240; 509pp; English.
                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                       expressed sequence tag; gene; ss
                                                                                                                                                                                                                                                                         ABN59829 standard; cDNA; 2992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-2001; 2001WO-US26015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-2000; 2000US-0659671
                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-292408/33.
P-PSDB; ABB97416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2992 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200222660-A2
                                                                                                                                                                                                           CAA 2908
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                  CAA 303
                                                                                                                                                                                                                                                                                                                             28-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention
                                                                                                                                                                                                                                                                                                  ABN59829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoded
                                                   2726
                                                                            181
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DB 24; Length 2992;

Score 296.6; DB 2. Pred. No. 1.1e-88;

59.2%;

Best Local Similarity

Query Match

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primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                            2979
                                                                                                                                                        2859
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                                2739
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                                                             120
                                                                                                                         180
                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
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                              2680 GGTATGGAGCTGTGCCGAGGCTTGGGGTCCCACATAAGCACTAGTCTATAGATGCCTCTT
                                                                                                                                         2860 CTCTAATCCAGCAAAATGATTCCCTGCACACAGAGACAAGCAGAGTAACAGGATCAGTG
                                                                                                                                                                                                                                                                2920 GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG
GGTATGGAGCTGTGGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT
                                                             ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCGCTTTC
                                                                                                                                                                                     CTCTAATCCAGCAAAGTGATTCCCTGCACACCAGAGACAAGCAGGAGTAACAGGTG
                                                                                                                                                                                                                                                 GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG
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Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID 11557; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nishikawa T, Hayashi K, S
T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA sequence SEQ ID NO:11557.
                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                        AAH14250 standard; cDNA; 2976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isoqai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                            2980 CAA 2982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1074617-A2
                                                                                                                                                                                                                                                                                                             CAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH14250;
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            complementary strand of a polymotheotide which comprises a 5'-end sequence and an oligonucleotide which comprises a 5'-end sequence and an oligonucleotide which comprises a 5'-end sequence complementary to a polymucleotide which comprises a 1'-end sequence complementary to a oligonucleotide comprises at 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polymucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13639 represent human cDNA sequences; ABB92446 to AAH13632 represent toligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2856 CTCTAATCCAGCAAAATGATTCCCTGCACCACAAGAAAAAGATAACAGGATCAGTG 2915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCTAATCCAGCAAAGTGATTCCCTGCACACCAGAGACAAGCAGAGTAACAGGATCAGTG 240
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                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     1 GGTATGGAGCTGTGCCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT 60
 an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                  DB 22; Length 2976;
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                                                                                                                                                                                                                                                                                                                            58.8%; Score 294.6; DB 22; Length 98.7%; Pred. No. 5e-88; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                             Sequence 2976 BP; 712 A; 807 C; 856 G; 601 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA clone (3'-primer) SEQ ID NO:7761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH10926 standard; cDNA; 481 BP.
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2000JP-0118776.
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2000JP-0241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 98.7
Matches 297; Conservative
                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 C 301
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                                                                                                                                                                                                                                                                                                                                  Query Match
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AAH10926/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 AGGACTGCTGCCTGCCACGCCCAGGACCAGGAGCTGCCACCACACAACAAGAAGA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 CTCTAATCCAGCAAAGTGATTCCCTGCACACAGAGAAGCAGAGTAACAGGATCAGTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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                                                          Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCACCTTTC
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                                                          Saito K, Ya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 481 BP; 99 A; 130 C; 114 G; 131 T; 7 other;
                                                                                                                                                                                                                                                           Claim 3; SEQ ID 7761; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 293.6; DB
Pred, No. 4e-88;
); Mismatches
                                                                             Nagai K,
                                                        Hayashi P
A, Nagal
                                                                             Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS99133 standard; cDNA; 2892 BP.
                                                  sogai T, Nishikawa T,
Sugiyama T, Wakamatsı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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98.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the present invention.
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Matches 296; Conservative
                  (HELI-) HELIX RES INST.
                                                                                                                   WPI; 2001-318749/34.
                                                                                                                                                                                                                     full-length cDNAs -
                                                          Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C 301
                                                                             Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 C 1
                                                        Ota T,
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2830 GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG 2889
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                                                                                                                                RESULT 13
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                                      οy
                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a human prostate cancer predisposing gene coding for an HPC2 polypeptide. The DNA and protein sequences are useful as diagnostic reagants for identifying a mutant HPC2 nucleotide sequence in a suspected mutant HPC2 allele by comparing the sequence of the suspected mutant HPC2 allele with a wild-type HPC2 sequence. The sequences are also useful for detecting an alteration in HPC2, where the alteration is associated with cancer in a human. The method involves analysing an HPC2 gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in HPC2 gene is useful as a marker for prostate cancer and can be used in which carry the mutant HPC2 allele. The sequences represent primers used in the methods of the invention, cDNA encoding human and mouse HPC2 and cDNA encoding HPC2 paralogues and orthologues.
                                                                                                           HPC2; prostate cancer; neoplastic growth; cytostatic; ss; prostate cancer predisposing gene; chimpanzee; gorilla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2770 CTCTAATCCAGCAAAGTGATTCCCTGCACCACCAGAGACAAGCAGAGTAACAGGATCACTG 2829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ACTAATTTCAATGCCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCACCTTTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCTAATCCAGCAAAGTGATTCCCTGCACACCAGAGACAAGCAGAGTAACAGGATCAGTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for prostate cancer, is useful in gene therapy techniques to restore HPC2 normal levels by which neoplastic growth is suppressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGTATGGAGCTGTGCCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2606 GGTATGGAGCTGTGCCGAGGCTTAGGCTCCCACATAAGCACTAGTCTATA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.8%; Score 254.6; DB 24; Length 2892; 93.4%; Pred. No. 1.4e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2892 BP; 704 A; 787 C; 815 G; 586 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                               Rommens JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 92; Page 204:207; 239pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             Tavtigian SV, Teng DHF, Simard J,
                                                                                                                                                                                                                                                                                                                                                                                         (HOSP-) HOSPITAL FOR SICK CHILDREN.
                                                                                                                                                sequencing primer; PCR primer.
                                                                                                                                                                                                                                                                                                07-MAY-2001; 2001WO-US14602.
                                                                                                                                                                                                                                                                                                                                   05-MAY-2000; 2000US-0564805.
                                                                                                                                                                                                                                                                                                                                                                        MYRI-) MYRIAD GENETICS INC
                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 283; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-066599/09.
                                                                       Gorilla ELAC2 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAU73593
                                                                                                                                                                                   Gorilla gorilla
                                                                                                                                                                                                                       WO200185911-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recipient cell
                                                                                                                           qene therapy;
                                    12-MAR-2002
                                                                                                                                                                                                                                                            15-NOV-2001
AAS99133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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The invention relates to isolated polynucleotide (1) and polypeptide (II) sequences. (I) is useful as hybridisation probes, and yeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, generates or other traits to assess browserty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #8011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 204; DB 23; Pred. No. 9.6e-58; O; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 8011; 103pp; English.
                                                                                                                                                                                                                                                                 AAS72207 standard; cDNA; 1402 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 40.7%;
Best Local Similarity 97.6%;
Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-639362/73.
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                                               111
2890 CAA 2892
                                                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
301 CAA 303
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Sequence 386 BP; 82 A; 90 C; 111 G; 103 T; 0 other;

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The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotides and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and the products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and proventive interventions. The polynucleotides and proventive interventions. The polynucleotides and proventive them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia, dysplasia and hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Innis MA, Garcia PD, Klinger J, Kassam A;
Kennedg GC, Pot D, Lamson G, Drmanac R;
Dickson M, Labat I, Leshkowitiz D;
LW, Strache-Crain B;
                                                                               AAGTCTTGGAAACAGACGGCGCCCCTTTCCTCTAATCCAGCAAAGTGATTCCCTGCACA 210
                                                                                                                            CCAGAGACAAGCAGAGTAACAGGGTCAGGGTCTAAGTGTCCGAGACTTAACGAAAATA 270
GGAGGCTGCCACACGGAAGCAAGCAGATGAACTAATTTCATTTCAAGGCAGTTTTTAAAG 150
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or
                                                                                                                                                                                                                                                                                                                                                                                                                           breast cancer; lung cancer; cancer detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences -
                                                                                                                                                                                                      Novel human polynucleotide, SEQ ID NO: 42.
                                                                                                                                                                                       GTATTTCAGCTGCAATAAAGATTGAGTTTGCA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 550-551; 1046pp; English.
                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                   AAF64286 standard; cDNA; 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000; 2000WO-US18374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0142310.
99US-0142311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams LT, Escobeuce, Reinhard C, Randazzo F, I
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-091805/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200102568-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                AAF64286;
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 91
                                                              151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  imaging of fittes expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                   GTACCCGGGTGGCTTGGAAGAAGTCAGCTCCGTCGTAGTGAGCACCTCTGGAACCTGTC 463
                                                                                                                                                     344 AGGGTCTGCTGTGCACCATCCTTGGAGAAGGCTCTCTGTGCTGTAGTGTGGCAGCTGCTG 403
                                   Gaps
                                                                                 and to produce other types of data and products dependent on DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                 ö
 Length 386;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            ONA encoding novel human diagnostic protein #8012.
Score 158; DB 22;
Pred. No. 1.4e-42;
                                                                                                                                                                                                                       CTCAGAGAGCCACCCTTATTCGCCAAGTCTTTTGACA 501
                                 Mismatches
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                                                                                                                                                                                                                                                                                                                         AAS72208 standard; cDNA; 1450 BP
31.5%; Scc
lilarity 100.0%; Pr
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73.
                Similarity
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                                 Matches 158;
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Query Match
                     Local
                                                                                                                                   404
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CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC Specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1450 BP; 355 A; 382 C; 418 G; 294 T; 1 other;
SQ Sequence 1450 BP; 355 A; 30.9%; Score 155; DB 23; Length 1450;
Best Local Similarity 87.8%; Pred. No. 2.9e-41;
Matches 273; Conservative 0; Mismatches 25; Indels 13; Gaps 9;
CONSERVATION OF GRAGGTGTGCCATARAGGATGCTTATAGATGCTTATAGG 63
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q ò	1026		1085
q	1086	1086 GAACTGGTGCCCTGGCACAGCTGCCCACACGCACGAAGCAGCAGAT 1145	1145
٥y	119	119 GAACTAATTTCATTT-CAAGGCAGTTTTTAAAG-AAGTCTTGGAAACAGACGGCGCCACC 176	176
qq	1146	GAACTAATTTCATTTCCAAGGCAGTTTTTAAAGAAAGTCATGGAAACAGACGGCGGCACC 1205	1205
οy	177	177 TTTCCTCTAATCCAGCAAAGTGATTCCCTGCACCACCAGAGACAAGCAGA-GTAACAGGAT 235	235
qq	1206	TTTCCTCTAATCCAGCAAAATGATTCCCTGCACACCAGAGACAAGCAGGGGTAACAGGT	1265
οy	236	236 CAGTGGGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAG-CTGCAATAAAGAT	292
qq	1266	1266 CAAGTGGGTCTAAAGTGTCCGAGACTTAACGAAAATAGTATTCCAGTCTGCAATAAAGAT	1325
Qy	293	293 TGAGTTTGCAA 303	
qq	1326	1326 TGAGTTTGCAA 1336	

Search completed: May 16, 2003, 03:40:57 Job time: 188.593 secs

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Sequence:

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Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; ss; gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla; sequencing primer; PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate cancer predisposing gene (HPC2) cDNA coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rommens JM;
                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                         ABQ15915
AAS98940
                                                                                                                                                                                                                              AAS99125
AAS98928
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AAL16688
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AAS98929
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AAS98932
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                 AAS72208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MYRI-) MYRIAD GENETICS INC.
(HOSP-) HOSPITAL FOR SICK CHILDREN.
                                                                                               AAS7
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                                                                                                                                                                                                                                                                                                                                                                               AAS98916 standard; cDNA; 2481
 07-MAY-2001; 2001WO-US146Q2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAY-2000; 2000US-0564805
                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Favtigian SV, Teng DHF,
WPI; 2002-066599/09.
P-PSDB; AAU73586.
WO200185911-A2.
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                                                                             1645.6
1080.8
518.2
475.8
247.4
247.4
247.4
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AAS98916
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il nucleic acid sequence encoding HPC2 polypeptide, which is marke prostate cancer, is useful in gene therapy techniques to restore inormal levels by which neoplastic growth is suppressed in cell recipient Novel HPC2 for

Claim 2; Page 128-131; 239pp; English.

The invention relates to a human prostate cancer predisposing gene coding for an HPC2 polypeptide. The DNA and protein sequences are useful as diagnostic reagents for identifying a mutant HPC2 nucleotide sequence in a suspected mutant HPC2 allele by comparing the sequence of the suspected mutant HPC2 allele by comparing the sequence. The sequences are also useful for detecting an alteration in HPC2, where the alteration is associated with cancer in a human. The method involves analysing an HPC2 gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in gene therapy techniques to suppress neoplastic growth of recipient cells which carry the mutant HPC2 allele. The sequences represent primers used in the methods of the invention, cDNA encoding human and mouse HPC2 and cDNA encoding HPC2 and

ö 180 120 180 240 300 360 420 420 480 480 540 540 300 360 9 600 999 Gaps 9 9 ACCATATCGCAGGCACCCGCCGCGCGAGGGCCGCGCAAGGACCCGCTGCGGCACCTG ATGTGGGCGCTTTGCTCGCTGCTGCGGGCCGGCCGGACGCACCATGTCGCAGGGACGC CGCACGCGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCCAAACACCGTGTACCTG CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCGTCTACGTCTTCTCCGAGTTC **AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA** GAGCCACACCTTCCACATGGTGTTAGCCAGAGAGAGGGGGTCAGGGACTCTTCCCTGGTC **AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC** ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA GAAAGGCCTCTCAGCAGGCTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT . 0 DB 24; Length 2481; Indels Sequence 2481 BP; 588 A; 686 C; 711 G; 496 T; 0 other; ö Score 2481; I Pred. No. 0;); Mismatches ; 0 08; Query Match
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design; ss
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gene therapy; peptide therapy; drug
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cancer predisposing gene HPC2, which is found on chromosome 17p. Some alleles of this gene cause a predisposition to cancer, particularly prostate cancer. This gene and its protein can be used in peptide and gene therapy for cancer patients, as well as being useful as diagnostic tools (both for cancer sufferers and those with a predisposition to the disease) and in the production of cancer drugs. This sequence was isolated by cloning and sequencing the region of the genome which appeared to cause a predisposition to prostate cancer.
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δŏ	Oy Oy	qq	QY Dp	ý á	7 7	OY Db	QY	Qy	Q P	Qy Db	oy Dp	oy Og	Qy	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Οy

use; HPC2; prostate cancer; neoplastic growth; cytostatic; ss; rapy; prostate cancer predisposing gene; chimpanzee; gorilla; ng primer; PCR primer. 1860 1910 2040 2100 2210 AAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280 2340 2510 1920 1970 2090 2160 2220 2270 2400 2450 GCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGGCC 2460 TIGAACCACTTCAGCCAGGGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGCCCCAACTTCAGCCCCAACTTCAGCCCCAACTTCAGCCCCAACTTCAGCCCAACTTCAGCCCAACTTCAGCCCCAACTTCAGCCCAACTTCAGCCCAACTTCAGCCCAACTTCAGCCCAACTTCAGCCCAACTTCAGCCCAACTTCAGC **ATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA** TCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG :ACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT AGGGAGAAGCGGGAGCTGCGGCGGCGGCCCTCCTGTCCAGGGAGCTGGCA AACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 3TCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC AGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG ostate cancer predisposing gene (HPC2) extended cDNA. standard; cDNA; 2958 BP AAGGTCAGAGCCCAGTGA 2481 002 (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a human prostate cancer predisposing gene coding for an HPC2 polypeptide. The DNA and protein sequences are useful as diagnostic reagatus for identifying a mutant HPC2 nucleotide sequence in a suspected mutant HPC2 allele by comparing the sequence of the suspected mutant HPC2 allele with a wild-type HPC2 Sequence. The sequences are also useful for detecting an alteration in HPC2, where the alteration is associated with cancer in a human. The method involves analysing an HPC2 gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in HPC2 gene is useful as a marker for prostate cancer and can be used in which carry the mutant HPC2 allele. The sequences represent primers used in the methods of the invention, CDNA encoding human and mouse HPC2 and CDNA encoding HPC2 and
                                                                                                                                                                                                                                                                                                Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker for prostate cancer, is useful in gene therapy techniques to restore HPC2 normal levels by which neoplastic growth is suppressed in recipient cell -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2958 BP; 707 A; 805 C; 848 G; 598 T; 0 other;
                                                                                                                                                                                                   Rommens JM;
                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 134-136; 239pp; English.
                                                                                                                                                                                                   Simard J,
                                                                                                                                    MYRIAD GENETICS INC.
HOSPITAL FOR SICK CHILDREN.
                                                          07-MAY-2001; 2001WO-US14602
                                                                                                 J5-MAY-2000; 2000US-0564805
                                                                                                                                                                                                   Teng DHF,
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(HOSP-) HOSPITA
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                  15-NOV-2001
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·; ACCATATCGCAGGCACCCCCCCCCCGCGAGCGGCCGCAAGGACCCGCTGCGGCACCTG 120 180 230 240 290 300 350 360 410 420 470 480 Gaps CAGGIGGIGGCAGCGGGACTCGGGCGCCGCGCCTCTACGTCTTCTCCGAGTTC AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGGC TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA DB 24; Length 2958; ö Indels ; s; Score 2481; I s; Pred. No. 0; 0; Mismatches Query Match 100.0%; Best Local Similarity 100.0%; Matches 2481; Conservative 0; 111 51 171 181 231 241 471 61 121 291 301 351 411 421 361 á g δy q ò Ω ò qq ŏ g ŏ qq δ С ò

οy	8	ATAGAACTGGCTGTGCGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540
qq	531	TAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 59
Qy Dp	541	TACCAGATCCCCATACACAGTGAACAGGGGGGAAAGCACCAACCA
Qy	0	AAAGGCCTCTCAGCAGGTCAGTCCAGAGCGATCTTCAGACTCGAGTCGAATGAAAT 66
qa	651	
٥y	661	AGCCACACCTTCCACATGGTGTTAGCCAGAGAGGGGGTCAGGGACTCTTCCCTGGTC 72
qa	711	CCACACCTICCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 77
oy g	01 1	TTAAAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 7
2	_	IAGUITICAICIGIAAGCITCACITAAAGAGGAAACITCITGGIGCICAAAGCAAAG
g g	781	GAGATGGGCTCCCAGTTGGAACAGTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840
Qy	4	SAAAAGCATCACTCATGAAGGAAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 90
qa	891	
QY	0	
qq	951	atcetegtectettttgtegtegtagaatgtccagatgaaacttcattcaacccat
QY	o	CCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCC
QΩ	1011	BAGAATGCCACCTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCTTGGT
Οy	1021	DACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGA
QQ	1011	acardececeaecarcrerecrescaeaeaeaeaeaeaeaeaeaeaeaeaeaeaeaeaeaea
Qy	1081	SGGCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 11
δý	4	GCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 120
Dp	6	
Qγ	1201	CAGTITCCGCTGTAAGAAGGAGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 12
QQ	1251	STTTCCGCTGTAAGAAGGAGG
δλ	56	SAGTACCAGCTCCGTCCCAGGAGGAGTGGCAGAGGGATGCCATTATTACT.
a D	31	GCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 137
Oy	32	ATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGGCGTG 138
qq	1371	CAATCCTGAGGAATTCATAGTTGAGGGGGTGCAGCTTCCCAACTTCCAGCAGAGGGTG 1.
Οy	1381	3ACGGCCCAGCCCCAGCAGAGAAAG
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δ, d		GGCTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 150
2	,	CAGAAAICAICIICCIIGGAACAGGGICIGCCAICCGAIGAAGAIICGAAAIGICAGI 133
Qy	0	56
Op	1551	CCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCAC

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                                                                   GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG
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The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTS). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat fifertility, to regulate haemastasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
                                                                therapy;
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human coding sequence SEQ ID NO: 240
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100.0%; Pred. No. 0;
tive 0; Mismatches
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Wehrman T,
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Best Local Similarity 100.
Matches 2481; Conservative
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Xue AJ, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
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                                                                                                                                                           Homo sapiens
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28-JUN-2002

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Db 1515 CCAGAAATCAT	Qy 1501 GCCACACTTGTV	Qy 1561 TTTGGGCAGCT Db 1635 TTTGGCCAGCT	Oy 1621 GCTGTGTTTGT Db 1695 GCTGTGTTTGT	Qy 1681 CAGAGAGACG 	Qy 1741 CCCAACCAGGTr 	Qy 1801 CACATCAGTAT' 	Qy 1861 GTGGAAAGATT 	1921	Qy 1981 GTGGTCTATTC Db 2055 GTGGTCTATTC	Oy 2041 ACCCTCCTGAT.	Oy 2101 ACACACAGCAC.	Qy 2161 ATGCTGAACCA 	Qy 2221 GAGAAAGTGGG 	Oy 2281 CCCAAGCTGAT' Db 2355 CCCAAGCTGAT'	Qy 2341 CGCAGGAGAA Db 2415 CGCAGGAGAA	Qy 2401 GGCGGCTGGA 	0y 2461 AAGAAGGTCAG. 	RESULT 5 AAA52810
	CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 4	481 ATAGAACTGGCTGTGGGCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540 	TACCAGATCCCCATACACAGTGAACAGAGGGGGAAAGCACCAACCA	601 GAAAGGCCTCTCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660 		721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780 }	781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840	841 GGGAAAAGCATCATGAAGGAAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900 	901 GATCCTGGTGCTGTTTGTGGTGGTGGAATGTCCAGATGAAAGCTTCATTCA		1021 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGA				1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGAGTGGCAGGGGTGCCATTATTACT 1320 	1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCGAGCG	1381 CAGGAGTACAGGAGGAGGGCGCAGGCCCAGCAGCAGAGAAAGAA	1441 CCAGAAATCATCTTCGTTGGAACAGGGTCTGCCATCCGATGAAGATTCGAAATGTCAGT 1500
පු	Oy Dp	Qy Db	Oy Db	çy GD	Qy Db	Qy Db	Oy Db	Qy Db	Oy Dp	Qy Db	O.y Db	Qy Db	Qy	Qy Db	Qy Dp	Qy Db	Qy Db	Qy

1620 1680 1754 1740 1814 1800 1874 1920 1994 1980 2040 2114 2100 2174 2160 2234 2220 2294 2340 2414 2460 1634 1694 TGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860 AGCGGGAGCTGCGGCAGGTGCGGCCGCCCTCCTGTCCAGGGAGCTGGCA 2400 ICTICCTIGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1574 TCAAAGCCTGGCTCCAGCAGTACCACAACCAGGGCCAGGAGGTCCTGCAC ACTTCAGCCAGGGCTATGCCAAGGTCCCCTCTTCAGCCCCAACTTCAGC SCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC IGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT CCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC TACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG CAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT TTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG AGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC TGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG IGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCTGGCT 111111111 GAGCCCAGTGA 2555 SAGCCCAGTGA, 2481

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Pred. No. 0;
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CDNA;
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                                                                      TTAAGTGGAATGATTCTTAAAAGGAAACCGGGCTTCCAAAGTGTACTTTCTGGA
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                                                                                                                            CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT
                                                                                                                                                           1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT
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                                                              TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT
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The invention relates to a human prostate cancer predisposing gene coding for an HPC2 polypeptide. The DNA and protein sequences are useful as diagnostic reagants for identifying a mutant HPC2 nucleotide sequence in a suspected mutant HPC2 allele by comparing the sequence of the suspected mutant HPC2 allele with a wild-type HPC2 sequence. The sequences are also useful for detecting an alteration in HPC2, where the alteration is associated with cancer in a human. The method involves analysing an HPC2 gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in
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Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; s: gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla; sequencing primer; PCR primer.
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Otsuki
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAX-2000; 2000JP-0183767.
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the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13528 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
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0; Mismatches
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Best Local Similarity 99.7%;
Matches 2474; Conservative
                                                                               the present invention.
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Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker for prostate cancer, is useful in gene therapy techniques to restore HPC2 normal levels by which neoplastic growth is suppressed in recipient cell
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  GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG
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English 204-207; 239pp; Page 92; Claim

The invention relates to a human prostate cancer predisposing gene coding for an HPC2 polypeptide. The DNA and protein sequences are useful as diagnostic reagents for identifying a mutant HPC2 nucleotide sequence in a suspected mutant HPC2 allele by comparing the sequence of the suspected mutant HPC2 allele with a wild-type HPC2 sequence. The sequences are also useful for detecting an alteration in HPC2, where the alteration is associated with cancer in a human. The method involves analysing an HPC2 gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in gene therapy techniques to suppress neoplastic growth of recipient cells which carry the mutant HPC2 allele. The sequences represent primers used in the methods of the invention, cDNA encoding human and mouse HPC2 and

ó 120 120 180 180 240 240 300 300 360 360 420 420 480 480 540 540 600 009 999 999 720 780 780 Gaps 9 9 ACCATATCGCAGGCACCGGCGCGCGGGGGGGGGGGGGGAAGGACCCGCTGCGGCACCTG CGCACGCGAGAGAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCCGTGTACCTG CAGGTGGTGCCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAAAAT GAGCCACACCTTCCACATGGTGTTAGCCAGAGAGGGGGTCAGGGACTCTTCCCTGGTC GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGGAAACTTCTTGGTGCTCAAAGCAAAG ATGTGGGGGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC ; 0 DB 24; Length Indels Sequence 2892 BP; 704 A; 787 C; 815 G; 586 T; 0 other; 24; encoding HPC2 paralogues and orthologues. Score 2442.6; Pred. No. 0; 0; Mismatches 98.5%; Conservative Query Match Best Local Similarity Matches 2457; Conserv in the concorn 541 241 61 121 121 181 181 241 301 301 361 361 421 421 481 481 601 199 199 721 721 61 501 $\overset{\mathsf{M}}{\times}\overset{\mathsf{$ ö g ò g ò 요 οy qq ΩŽ g δy QQ δλ Op δ g Qγ g δ g οy 8 δy g οý qq

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us-09-434-382-1.rng

frame

Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -

31-MAR-1999; 99US-0127607. 02-APR-1999; 99US-0127636. 05-APR-1999; 99US-0127728. 30-MAR-2000; 2000US-0540763.

(CURA-) CURAGEN CORP

Shimkets RA,

WPI; 2000-602362/57. P-PSDB; AAB42236.

31-MAR-2000; 2000WO-US08621

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vulnerary; antipsoriatic; antiparkinsonian; orderic; reprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunosuppressant; cardiant; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiflammatory; antiviral; artibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; allergy; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; ss.
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                                                                                                                                            ATGCTGAACCACTTCAGCCAGGGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC
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                                                              ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG
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                                                                                                                            GIGGICTATICCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC
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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; cities antiparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; Immunostimulant; cardiant; thrombolytic; coadilant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antihinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antihinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antihinflammatory; antibacterial; antiviral; in the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis; graft vs host disease, cardatovascular disease, disorders, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, hoperansion, hypothyroidism, cholesterol ester storage, systemic lupus concernal neamoglobinuria, antihiflammatory disease; to enhance concerns and individual concerns and cartilage damage, concerns and manage, concerns the enhance concerns and contiliage damage, concerns and cartilage damage, concerns and contiliage damage, concerns and contiliage damage, concerns and contiliants and contilian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
71.8%; Score 1782; DB 21; Length 2546;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 15; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coagulation; to inhibit thrombosis; and as a contraceptive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 3179-3180; 5507pp; English.
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AACCCATCTGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCGTGG	CCTTGGTGGTTCACATGGCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGA 	TGGAGAGGTTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTC 	ACAACCTTCGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCGGACATCTTCC	CCCTGCTCACCAGTTTCCGCTGTAAGAAGAGGCCCCACCCTCACTGTGCCCATGGTTC	AGGTGAATGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAG	TTATTACTTGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTGCCAACTTCCAGC	AGAGCGTGCAGGAGTACAGGAGGAGGCGCAGGCCCCAGCCCAGCCCAGCAGAAAAAA	GTCAGTACCCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCGGATGAAGATTGGAA 	ATGTCAGTGCCACACTTGTCAACATAAGCCCCGACACGTCTTCTGCTACTGGACTGTGGTG	AGGCACATTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCA 	CCCTGGCTGCTGTGTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTA	TCTTGCTGCTGCAGAGAGGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGG	TGGTTGCCCCCAACCAGGTCAAAGCTGGGTCCAGCAGTACCACAACCAGTGCCAGGGGG 	TCCTGCACCACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCA 	GTCCTGCAGTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTC 	AGACCTGTCTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACCTCTG	GCTGGAAAGTGGTCTATTCCGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGA 	AAGATGCCACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGAG
551	1013	1073	1133	1193	1253 851	1313	1373	1433	1493	1553	1613	1673	1733	1793	1853	1913	1973 1571	2033
QQ	Qy Dp	Qy Db	Qy Db	Qy Db	Q Dp	Oy Dp	Qy Db	Qy Dp	Oy Dp	Qy Db	Qy Db	Qy Db	Qy Db	Qy Dp	QY Db	Qy Db	Qy Db	Oy Db

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The invention relates to a human prostate cancer predisposing gene coding for an HPC2 polypeptide. The DNA and protein sequences are useful as diagnostic reagents for identifying a mutant HPC2 nucleotide sequence in a suspected mutant HPC2 allele by comparing the sequence of the suspected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; ss; gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla; sequencing primer; PCR primer.
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                                                                                                                                                                             1871 CAACAATGCCCCAAGCTGATTCCCCCCACTGAAAGCCCTGTTTGCTGGCGGCACATCGAGGAG 1930
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                                                                                                                                                                                                                                   Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker for prostate cancer, is useful in gene therapy techniques to restore HPC2 normal levels by which neoplastic growth is suppressed in recipient cell
               1691 TGGAAAAGACACACACACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCG 1750
 TGGAAAAGACACACACACACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGG 2152
                                                                                                                                                                                                                                                                         GAGCTGGCAGGCGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCAACACAGAGGAG 2451
                                                                    1751 AGTICATTATGCTGAACCACTTCAGCCAGGCGTATGCCAAGGTCCCCTCTTCAGCCCCA
                                                    AGTICATTATGCTGAACCACTTCAGCCAGGGCTATGCCAAGGTCCCCCTCTTCAGCCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MYRI-) MYRIAD GENETICS INC. (HOSP-) HOSPITAL FOR SICK CHILDREN.
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mutant HPC2 allele with a wild-type HPC2 sequence. The sequences are also useful for detecting an alteration in HPC2, where the alteration is associated with cancer in a human. The method involves analysing an HPC2 gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in gene therapy techniques to suppress neoplastic growth of rectipient calls which carry the mutant HPC2 allele. The sequences represent primers used in the methods of the invention, CDNA encoding human and mouse HPC2 and

4 CGCACCATATCGCAGGCACCCGCCCGCCGAGCGGCCGCGCAAGGACCCGCTGCGGCAC 117 177 153 237 213 297 273 357 333 417 393 477 453 537 513 597 573 657 633 717 678 777 837 897 858 957 Gaps 66 CTGCGCACGCGAGAGCGCGGACCGTCGGGGTGCTCCGGCGCCCCAACACGTGTAC CTGCAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCGCTCTACGTCTTCTCCGAG CTGCAGGTGGTGGCGGCGGGGGGGGCGGGGGGCTCCTCTATGTCTCTCGGAA TTCAACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAG GGAATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACA CCCAGAACATCTCCCAACAGGCTCAGTCCCAAACAGTCATCGGACTCTGGATCAGCTGAA TACAACAGGTACCTTTTTAACTGCGGAGAAGGCGTCCAACGACTTATGCAGGAACAAAG TTAAAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGG GGACCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAA GTTTACCAGGTCCCTATCCACAGTGAACGGAGGTGTGGAAAGCAACAGCCATCCCAGAGC CCAGAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAA **AATGAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGGTCAGGGACTCTTCCCTG** GTCGTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAAGGAAACTTCTTGGTGCTCAAAGCA AAGGAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAG GACGGGAAAAGCATCACTCATGAAGGAAGAGATTTTGGCTGAAGAGCTGTGTACTCCT GCCTTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCT 24; Length 2470; 24; 0; Mismatches 417; Indels Sequence 2470 BP; 614 A; 664 C; 679 G; 510 T; 3 other; DB encoding HPC2 paralogues and orthologues. Score 1645.6; Pred. No. 0; Query Match
Best Local Similarity 81.6%;
Matches 1958; Conservative CDNA 28 40 118 100 154 238 214 274 334 619 739 178 298 358 418 478 454 538 514 598 574 658 634 718 778 838 199 868 394 QQ g οp g g g g ò g οy QQ g g g g q à ô δ δ Qγ Ω δ ò ò ò ô ŏ

1437 1497 1017 1077 1098 1197 1257 1218 1317 1278 1557 1518 1617 1578 1677 1737 1698 1797 1857 1818 1917 1878 1977 2037 918 978 CTTCGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCGGGACATCTTCCCCCTG ACTTGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGC AAAGTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCGGATGGGAAAGAT AGGTTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAAC CTGCGCAGCCACAAGATTCAGACCCAGCTCAGCCTCATCCACCCTGACATCTTCCCCCAG CTCACCAGTTTCCGCTGTAAGAAGGAGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGT GAATGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGGAGTGGCAGAGGGATGCCATTATT TATCCTGAAATTGTCTTCCTGGGTACGGGGTCTGCCATCCCAATGGAGATCCGAAATGTC ACATTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTG GCTGCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTG CTGCAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTT GCCCCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTG GCAGTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACC ATCTGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTG AGTGCCACACATTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGC CACCACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCT 1018 1039 1138 1099 1159 1258 1219 1318 1279 1378 1339 1438 1.399 1459 1558 1519 1618 1579 1678 1639 1738 1759 1858 1819 1918 1978 1798 1879 928 919 979 1078 1699 1198 1498 qq qq qq Dp qq g QQ ò Dp ò Db δ g οy PP δ g δλ g ο QQ ò g Óχ ò οy qq ÓΥ οy ò õ QQ óγ ò ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                         2217
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                                                                                                                                                                                                          AAAGTCGTCTACTCGGGGGATACCATGCCCTGTGAGGCTCTGGTCCAGATGGGGAAAGAT 1998
                                                                                                                                                                                                  2456
                                                                                                                                                                                                                                            1239 GTGCCCAAGCTGATTCCCCCACTGAAGGCCCTGTTTGCAGGTGACATTGAAGAGATGGTG
                2218 AGCGAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACA
                                                                                                                                                              2278 AIGCCCAAGCIGAITCCCCCACIGAAAGCCCTGTITGCIGGCGACATCGAGGAGATGGAG
                                                                                        ATTATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                     AAGACACACACACACGTCCCAAGCCATCAGCGTGGGGGATGCGGATGAACGCGGAGTTC
                                                                                                                                                                                                                                    GCAGGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACA
                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                       novel human diagnostic protein #8011.
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2000US-0649167.
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Second to produce data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1080.8; DB 2
Pred. No. 1.2e-265;
                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
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Matches 1173; Conservative (
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                                                 856
                                                                        TCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCCCCCCAACCAGCTCAAAGCCTGG
                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromo
                        CACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTGCAGAGAAGGCGCGCTTGGCA
                                    857 TCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTTGCCCCCCAACCAGCTCAAAGCCTGG
                                                                                                                      CTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCACCACATCAGTATGATTCCTGCC
                                                                                                                                    AAA-TGCCTTCAGGAAGG-GGCTGAGATCTCCAGTCCTGCAGTGGAAAGATTGA-TCAGT
                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diágnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                  encoding novel human diagnostic protein #8012.
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2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
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and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating of slood supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating of slood supplement. (II) and its binding partners are useful in medical calsorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in cresponsable for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human conding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO conding int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 518.2; DB 23; Length 1450;
Pred. No. 5.4e-122;
0; Mismatches 49; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                          Sequence 1450 BP; 355 A; 382 C; 418 G; 294 T; 1 other;
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90.3%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotide which comprises a 3'-end sequence, where the coligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sare useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs asily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13633 to AAH13639 to AAH3629 to AAH3628 represent human amino acid sequences; and AAH13629 to AAH3632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonuclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nuclectide sequences defined in the specification, where the oligonuclectide comprises at least 15 nucleotides; or (b) a combination of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynuclectide which comprises a 5'-end sequence and an oligonuclectide comprising a sequence complementary to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saito K,
Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 584 BP; 122 A; 166 C; 178 G; 115 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.2%; Score 475.8; DB 22; llarity 98.0%; Pred. No. 2.4e-111; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID 2670; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             likawa T, Hayashi K, Si
Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                     Human cDNA clone (5'-primer) SEQ ID NO:2670
2460 CAAGAAGGTCAGAGCCCAGTGA 2481
                            BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishikawa T,
                                                                                                                                                                      AAH05835 standard; cDNA; 584
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugiyama T,
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Best Local Similarity
Matches 491; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                    AAH05835;
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                                                861
                                                                                                                        RESULT 13
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HPC2; prostate cancer; neoplastic growth; cytostatic; ds; prostate cancer predisposing gene.
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                                                                                                                                                                                                                                                                                                                                                                                                   480
                                                                                                                                                                        240
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                                                                                                                                                                                                                                                                                    AAGGTIGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360
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                                                         ACCATATCGCAGGCACCCGCCGCGCGGGGCGCCGCGCAAGGACCCGCTGCGGCACCTG 120
                                                                                                             121 CGCACGCGAGAGAGAGCGCGGACCGTCGGGGGTGCTCCGGCGCCCCAAACACCGGTGTACCTG 180
                                                                                                                                           254
                194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostate cancer predisposing gene (HPC2) DNA full length exon
                                                                        CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACACGTGTACCTG
                                                                                                                                                                                                                              AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA
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                                                                                                                                                                     CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCGCTCTACGTCTTCTCCGAGTTC
ATGTGGGCGCTTTGCTCGCTGCTGCGGGCCGGCCGGACGCACCATGTCGCAGGGACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAGAACTGGCTGTGCGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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recipient cell

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Gaps

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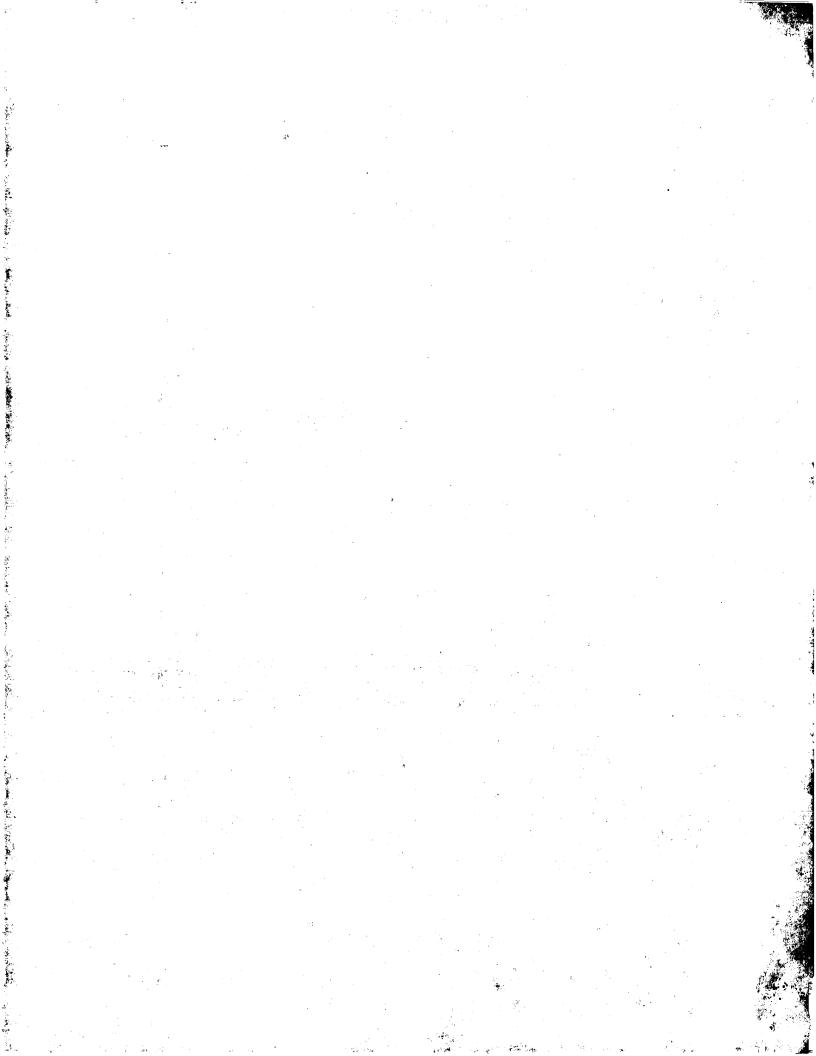
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   The invention relates to a human prostate cancer predisposing gene coding for an HPC2 polypeptide. The DNA and protein sequences are useful as diagnostic reagents for identifying a mutant HPC2 nucleotide sequence in a suspected mutant HPC2 allele by comparing the sequence of the suspected mutant HPC2 allele by comparing the sequence of the suspected mutant HPC2 allele with a wild-type HPC2 sequence. The sequences are also useful for detecting an alteration in HPC2, where the alteration is associated with cancer in a human. The method involves analysing an HPC2 gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in gene therapy techniques to suppress neoplastic growth of recipient cells which carry the mutant HPC2 allele. The sequences represent DNA encoding
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                                                                                                                                                                                                                                                                                                                                           121 CGCACGCGAGGAGGGGGGCGGACCGTCGGGGTGCTCCGGCGGCCCCAAACACCGTGTACCTG 180
                                                                                                                                                                                                                                                                61 ACCATATCGCAGGCACCCGCCGCGCGGCGGCGGCGAAGGACCCGGCTGCGGCACCTG 120
                                                                                                                                                                                                                          9
                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                 1 ATGTGGCGCGTTTGCTCGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prostate cancer predisposing gene; HPC2; chromosome 17p;
gene therapy; peptide therapy; drug design; ds.
                                                                                                                                                                               Query Match

10.0%; Score 247.4; DB 24; Length 350;
Best Local Similarity 97.7%; Pred. No. 4.1e-53;
Matches 251; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate cancer predisposing gene HPC2 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "this sequence contains introns"
/transl_except= (pos:23892..23895,aa:Glu)
910..1154
                                                                                                                                                            Sequence 350 BP; 47 A; 125 C; 126 G; 52 T; 0 other;
                                                                                                                                                                                                     0; Mismatches
                                                                                                                                          human and mouse HPC2 and fragments of HPC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
          Example 5; Fig 4; 239pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA60207 standard; DNA; 26664 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "HPC2"
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1925..1995
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(MYRI-) MYRIAD GENETICS INC.

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                                                                                                                                                  Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies, useful for treatment and diagnosis of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; Length 26664;
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26664 BP; 6173 A; 6300 C; 6519 G; 7661 T; 11 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.0%; Score 247.4; DB 21; Best Local Similarity 97.7%; Pred. No. 2.7e-52; Matches 251; Conservative 0; Mismatches 6;
                                                      Teng DHF, Simard J, Rommens JM;
                                                                                                                                                                                                     Claim 3; Page 108-122; 157pp; English
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Job time : 574.621 secs
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                                                                                         WPI; 2000-376481/32
                                                                                                             P-PSDB; AAB07228
                                                      Tavtigian SV,
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APPLICANT: Tartigian, Sean V.
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APPLICANT: Tartigian, Seau V.
APPLICANT: Simard, Jacques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ 1D NOS: 240
SOFTWARE: Patentin Ver. 2.0
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US-08-725-459B-1
US-09-231-061-2
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Best Local Similarity
Matches 826; Conserv
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US-09-564-805-220
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US-09-54-805-231
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Patent No. 6333403

GENERAL INFORMATION:
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Jaques
APPLICANT: Taminard, Jaques
APPLICANT: Time Jarques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 224
LENGTH: 826
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; ORGANISM: Pan troglodytes
US-09-564-805-224
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
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QVVAAGSRDSGAALYVFSEFNRYLFNCGEGVQRLMQEHKLKVARLDNIFLTRMHWSNVGG
                                                                     LSGMILTLKETGLPKCVLSGPPQLEKYLEAIKIFSGPLKGIELAVRPHSAPEYEDETMTV
                                                                                                                                           YQIPIHSEQRRGKHQPWQSPERPLSRLSPERSSDSESNENEPHLPHGVSQRRGVRDSSLV
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CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 226, Application US/09564805; Patent No. 6333403; GENERAL INFORMATION:
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APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
FILE REFERENCE: 2318-258
CURRENT PAPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 1000-05-05-05
PRIOR PILING DATE: 1998-11-06
PRIOR PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 222
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Pred. No. 0;
66; Mismatches
         Teng, David H.F.
Simard, Jacques
Rommens, Johanna M.
                                                                                                                                                                                                                                  80.3%;
80.5%;
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                 ; ORGANISM: Mus musculus US-09-564-805-222
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Matches 665; Conserv
          APPLICANT: APPLICANT: APPLICANT: 1
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                                                                       Length 826;
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                                                                     Score 4261; DE Pred. No. 0; 5; Mismatches
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Patent No. 6333403
GENERAL INFORMATION:
                                                                     Match 98.5%;
Local Similarity 98.5%;
les 814; Conservative
                            TYPE: PRT
ORGANISM: Gorilla gorilla
US-09-564-805-226
 Patentin Ver.
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SOFTWARE: Page 12 SEQ ID NO 226
                                                                     Query Match
Best Local S.
Matches 814
                    LENGTH:
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ORGANISM: Caenorhabditis elegans
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LENGTH: 844
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APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tartiglan, Sean V.
APPLICANT: Sinard, Jacques
APPLICANT: Sinard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Wriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
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                          IMLNHFSQRYAKVPLFSPNFSEKVGVAFDHMKVCFGDFPTMPKLIPPLKALFAGDIEEME 779
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                                                                                       ERREKRELRQVRAALLSRELAGGLEDGEPQQKRAHTEE---PQAKK 822
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                                                                                                                                                                                 Sequence 228, Application US/09564805 Patent No. 6333403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-564-805-228
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SOFTWARE: Patentin Ve
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                                                          GEGTFGQLCRHYG-DQVDRVLGTLAAVFVSHLHADHHTGLPSILLQRERALASLGKPLHP
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Patent No. 6333403

GRBERAL INFORMATION:
APPLICANT: Tavitigian, Sean V.
APPLICANT: Tavitigian, Sean V.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Suscepi;
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Suscepi;
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE OF INVENTION: Gene and a Paralog and Orthologous Genes
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FILE OF INVENTION: GENERAL G
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	QY 236 DSSLVVAFICKLHLKRGNFLVLKAKEMGLPVGTAAIAPIIAAVKDCKSIT-HEGREILAE 294 :::: :: :: :: : Db 242 VNNVDIAFLIEMKEAARRIDTMKLMELKVPKGPLIGKLKSGEAVTLPDGRTIQPD 296	QY 295 ELCTPPDPGAREVVVECPDESFIQPICENATFORYOGKADAPVALVVHMAPASVLVD 351 297 QVFSSDKVEGDKPLLLVTECTTEDHVKALIDSSSLQPFL-NGEKQLDYMVHISDDAVINT 355	QY 352 SRYQQWMERF-GPDTQHLVLNENCASVHNLRS-HKIQTQLNLIHPDIFPLLTSFRCKKEG 409 15	QY 410 PTLSVPMYQGECLLKYQLRP-RREWQRDAIITCNPEEFIVEALQLPNFQQ 458 1	QY 459 SVQEYRRSAQDGPAPAEKRSQYPEIIFLGTGSAIPMKIRNVSATLVNISPDTSLLLDCGE 518 :: :: : : :	QY 519 GTFGQLCRHYG-DQVDRYLGTLAAVFVSHLHADHHTGLPSILLQRERALASLGKPLHPLL 577	QY 578 VVAPNQLKAWLQQYHNQCQEVLHHISMIPAKCLQEGAEISSP 619 1 :	QY 620AVERLISSL-LRTCDLEEFQTCLVRHCKHAFGCALVHTSGWKVVSGDTWPCEALVRM 676 1: 1 1 1 1 1 1 1 1 1 1	QY 677 GKDATLLIHBATLEDGLEEBAVEKTHSTTSQAISVGMRNNAEF 719	Qy 720 IMLNHFSQRYAKVPLFSPNFSEKVGVAFDHMKVCFGDFPTMPKLIFPPLKALFAGDIEE 777	Qy 778 MEBRREKRELR 788 : :: : 1: Db 821 LTIKKEQRVLK 831	RESULT 7 US-09-315-794-52 ; Sequence 52. Application US/09315794	Patent No. 6197517 GENERAL INFORMATION: APPLICANT: Roberts, Christopher J.	; TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL ; TITLE OF INVENTION: AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION ; TITLE OF INVENTION: DRUGS ; FITLE DEPENDENCE, 0201-052	CURRENT FILING DATE: 1999-05-21	; NUMBER OF SEQ ID NOS: 64 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 52 ; LENGTH: 838	; TYPE: PRT ; ORGANISM: Saccharomyces cerevisiae US-09-315-794-52	Query Match 13.9%; Score 599.5; DB 4; Length 838; Best Local Similarity 25.7%; Pred. No. 1.9e-49; Matches 221; Conservative 138; Mismatches 290; Indels 211; Gaps 36; Qy 82 RYLF-NCGEGVQRLMQEHKLKVARLDNIFLT-RMHWSNVGGLSGMILTLKETGLPKCVLS 139

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US-09-564-805-229
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LENGTH: 838
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                                                                                                                                                                                                         Indels 211;
                                                                                                                                                                   Length 838;
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13.9%; Score 599.5; DB 4;
Best Local Similarity 25.7%; Pred. No. 1.9e-49;
Matches 221; Conservative 138; Mismatches 290;
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                                                                                            ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-389-341-52
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 52
LENGTH: 838
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APPLICANT: Tavigian, Sean V.
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APPLICANT: Sinard, Jacques
APPLICANT: Sommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 RYLF-NCGEGVQRLMQEHKLKVARLDNIFLT-RMHWSNVGGLSGMILTLKETGLPKCVLS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 GPPQLEKYLEAIKIFSGPLKGIELAVRPHSAPE---YEDETMTVYQIPI---HSEQRRGK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 HQPWQS------PERPLSRLSPERSSDSESNENEPHLPHGVSQRRGVRDSSLVV 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 PPDPGAAFVVVECPDESFIQPICENATFQRYQGKADAPVALVVHMAPASVLVDSRYQQWM 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 DIFE-----KNNYGKVNHMISH-----NKISPNTISFFGSALTTLKLKALQVNNYN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 LPKTDRVFSKDFYDRFDTPLSRGTSMCKSQEEPLNTIIEKDNIHIFSQNKTVTFEPFRMN 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 KYFFGKIGEGSQRSLTENKIRISKLKDIFLTGELNWSDIGGLPGMILTIADQGKSNLVLH 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 462 --KKKHVEIITLGIGSALPSKYRNVSTLVKVPFTDADGNIINRNIMLDAGENTLGIHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---KCLQEGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 NERHFAKVLILDIPDDLYL-----NAFVEKFKDYDCAELGMYYYFLGDEVTINDNLFAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MFSQLAVKSIFQDLKMIYLSHLHADHHLGIISVL--NEWYKYNKDDETSYIYVVTP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 FDSFOKGVLRSIVAKMFPKHAPTDRYDP--SSDPHLNVELPDL------DAKVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERFGPDTQHLVLNENCASVHNLRSHKIQTQLNLIHPDIFPL----LTSFRCK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     407 --KEGPTLS------VPMVQGECLLKYQLRPRRE------WQRDAIITCNP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKRSQYPE11FLGTGSA1PMK1RNVSATLVN1----SPDTSLLLDCGEGTFGQLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409 EEPMKCNINGEVADFSWQEIFEEH-VKPLEFPLADVDTVINNQLHVDNFNNSAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels, 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.9%; Score 599.5; DB 4; Similarity 25.7%; Pred. No. 1.9e-49; 21; Conservative 138; Mismatches 290;
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; Sequence 229, Application US/09564805; Patent No. 6333403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae
                                                                  GENERAL INFORMATION:
APPLICANT: Tavtigi
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US-09-564-805-213
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                                                                                                                                                         SEQ ID NO 232
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LENGTH: 73
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APPLICANT: Tavijaian, Sean V.
APPLICANT: Tavijaian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jodques
APPLICANT: Simard, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-558
CURRENT FILING DATE: 2000-05-05
PRIOR PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1999-11-06
PRIOR APPLICATION NUMBER: 09/434,382
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
FERRICH APPLICATION OF 2.20
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APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Parene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
574 -W--QYHKFVNEWLVLENKEILKRIKKISCEHFINDSFVRMQTQSVPLAEFNEILKENSN 630
                                                                              SGWKVVYSGDIMPC--EALVRMGKDATLLIHEATLEDGLEEEAVEKTHSTTSQALSVGMR 714
                                                                                                                                                                                                            MNAEFIMLNHFSQRYAKVPLFSPN---FSEKVGVAFDHMKVCFGDFPTMPKLIPPLKALF 771
                                                                                                                                                                                                                                  1 MWALCSLLRSAAGRIMSQGRIISQAPARRERPRKDPLRHLRIREKRGPSGCSGGPNTVYL 60
                                                                                                                                                       -----EISSPAVER---LISSLLRTCDLEEFQTCLVRHCKHAFGCALV-----HT
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100.0%; Pred. No. 1.4e-33
Live 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 232, Application US/09564805 Patent No. 6333403 APPLICANT: Tavtigian, Sean V.
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Patent No. 6333403
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810 ---VEEKEEEEDVDDVESVQ 826
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Matches 81; Conserv
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APPLICANT: Tavtiqia
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TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REPERBENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR PRILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        538 TLAAVFVSHLHADHHTGLPSILLQ-----RERALASLGKP-LHPLLVVAPNQLKAWLQQY 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  482 EIIFLGTGSAIPMKIRNVSATLVNISPDTSLLLDCGEGTFGQLCRHYGDQVDRVLG---- 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 -HECIMKMGYFTLDFDINVHEVRGGTVVEEDDYRVTSAPASHSVFN--LAYCFEEKKRPR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: |||| ||:| | || :: : | | | |||||| |: : |
3 EVTFLGTSSAVPSKNRNHISIALRI-PGEIFLFDCGEGTQRQMA-----LAGISPM 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MWALCSLLRSAAGRTMSQGRTISQAPARRERPRKDPLRHLRTREKRGPSGCSGGPNTVYL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 IKLAEGAELLIHESTLEAGSEDKAAESGHSTAREAAEVARSAGVKRLILTHLSTRYKR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   674 VRMGKDATLLIHEATLEDGLEEEAVEKTHSTTSQAISVGMRMNAEFIMLNHFSQRYAK 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                            Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                         6:5%; Score 281; DB 4;
28.2%; Pred. No. 5.4e-19;
tive 45; Mismatches 93;
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Pred. No. 9.4e-20;
                                                                                                                                                                                                                                                                                                                           ORGANISM: Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.48;
74.18;
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Matches 84; Conservative
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Best Local Similarity
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Squence 221, Application US/09564805

Patent No. 6333403

GENERAL INFORMATION:

APPLICANT: Tavitigian, Sean V.

APPLICANT: Tavitigian, Jacques

APPLICANT: Sinard, Jacques

APPLICANT: Sinard, Jacques

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

FILE REFERENCE: 2318-28

CURRENT APPLICATION NUMBER: US/09/564,805

CURRENT APPLICATION NUMBER: US/09/564,805

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SOFTWARE: Patentin Ver. 2.0
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177 AFRLFHRIPSFGESVVEKKRPGKLNAQKLKDLGVPPGPAYGKLKNGISVVLENGVTISPQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      592 HNQCQEVLHHISMIPAKCLQEGAEI----SSPAVERLISSLLRT------CDLEEFQTC 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 DVLKKPIVGRKICILGD----CSGVVGDGGVKLCFEADLLIHEATLDDAQMDKAKEHGHST 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       482 EIIFLGTGSAIPMKIRNVSATLVNISPDTSL-LLDCGEGTFGQLCRHYGDQVDRVLGTLA 540
                                                                                                                                                                                                                                                                                                                                                  482 EIIFLGTGSAIPMKIRNVSATLVNISPDTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLAA 541
                                                                                                                                                                                                                                                                                                                                                                                                                                    542 VFVSHLHADHHTGLPSILLQRERALASIGKPLHPLLVVAPNQLKAWLQQ------Y 591
                                                                                                                                                                                                                                                                                                                                                                            658 ------GWKVVYSGDIMPCEALVRMGK-----DATLLIHEATLEDGLEEEAVEKTHST
                                                                                                                                                                                                                                                                                                          87;
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                                                                                                                                                                                                                                                               Length 363;
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                                                                                                                                                                                                                                                             5.7%; Score 245.5; DB 4; Length 26.4%; Pred. No. 2.1e-15; Live 42; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.6%; Score 243.5; DB 4
26.2%; Pred. No. 2.8e-15;
tive 46; Mismatches 132
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US 60/107,468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           641 LVR--HCKHAFGCALVHTS-----
                                                                                                                                                                                                                                                               Query Match 5.7%
Best Local Similarity 26.4%
Matches 87; Conservative
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84; Conservative
                                                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-09-564-805-220
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US-09-564-805-231
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US-09-564-805-23
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LENGTH: 326
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                                                                                                                                                           Sequence 230, Application US/09564805

Sequence 230, Application US/09564805

Patent No. 6333403

GENERAL INFORMATION.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tang, David H.F.

APPLICANT: Simard, Jacques

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

FILE REFERENCE: 2318-258

CURRENT APPLICATION NUMBER: US/09/564,805

CURRENT APPLICATION NUMBER: US 60/107,468

PRIOR PILING DATE: 1998-11-05

PRIOR FILING DATE: 1998-11-05

NUMBER OF SEQ ID NOS: 240

SEQ ID NO 230

LENGTH: 311
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Patent No. 6333403
GENERAL INFORMATION:
APPLICANT: Taviigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simart, Jacques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Ghee and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ----GKLDKIFISHLHGDHLFGLPGLLCSR-----SMSGIIQPLTIYGPQGIREFVETAL 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 476 KRSQYPEIIFLGTGSAIPMKIRNVSATLVNISPDTS---LLLDCGEGTFGQLCRHYGDQV 532
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                                                53 QVVAAGGRDAGAALYVFSEYN 73
                        61 QVVAAGSRDSGAALYVFSEFN 81
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US-09-564-805-230
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Qy	541	541 AVFVSHLHADHHTGLPSILLQRERALASLGKPLHPLLVVAPNQLKAWLQ 589
qq	57	RIFITHLHGDHIFGLMGLLASSGLAGSGQGIEIYGPEGLGDYLEACCRFSSTHLG 111
ΟÝ	290	SMIPAKCLOEGAEISSPAVE 622
qa .	112	KRLKVHTVRENGLIYEDKDFQVHCGLLKHRIPAYGYRVEEKQRPGRFNVEQAEALGIPFG 171
QY	623 j	RLISSLLRTCDLEBEROTCLVRHCKHAFGCALVHTSGWKVVYSGDTMPCEALVRMGKDA 680
ΩP	172	: PIYGQLKQGKTVTLEDGRRIRGQDLCEPPEPGRKFVYCTDTVFCEEAIALAQEA 225
Qy	681	TILIHEATLEDGLEEERAVEKTHSTTSQAISVGMRMNAEFIMLNHFSQRYAK-VPLFSPNF 739
qq	226 1	
Qy	740 8	SEKVGVAFDHMKVCFGDFPTM 760
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sequence 2, Application US/09988626

Sequence 2, Application US/09988626

Bublication No. US20030044959A1

GENERAL INFORMATION:
APPLICANT: Tavitigian, Sean V.
APPLICANT: Tavitigian, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Johanna M.
APPLICANT: Simard, Johanna M.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: 200-256

CURRENT APPLICATION NUMBER: US/09/988,626

PRIOR FILING DATE: 1999-11-05

PRIOR FILING DATE: 1999-11-05

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SEQ ID NO 2.

LENGTH: 826

TAVER: DATE: 1806

TAVER: DATE: 1806
        Sequence 213, App Sequence 230, App Sequence 220, App Sequence 220, App Sequence 211, App Sequence 211, App Sequence 6252, App Sequence 4, App 11 Sequence 915, App Sequence 915, App 11 Sequence 7, App 11 Sequence 2, App 11 Sequence 22, App 11 Se
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US-09-988-687-231
US-09-928-301-1076
US-09-928-301-1076
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US-09-9862-027-24
US-09-788-027-24
US-09-908-193-47
US-09-908-193-47
US-09-908-193-47
US-10-022-939-2
US-10-100-405A-2
US-10-100-405A-2
US-10-022-939-2
US-10-022-939-2
US-10-022-939-2
US-10-022-939-2
US-09-989-651-2
US-09-989-651-2
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US-10-033-245-22
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 826; Conservative 0; Mismatches
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US-09-988-626-2
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1: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
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Sequence 2, Application US/0998687

Publication No. US200300457041

GENERAL INPORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Mommens, Johanna M.
APPLICANT: Myriad Genefics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
CURRENT APPLICATION NUMBER: US/09/988,687

CURRENT FILING DATE: 2000-05-05

PRIOR FILING DATE: 2000-05-05
PRIOR PELLING DATE: 1999-11-05

PRIOR FILING DATE: 1999-11-05

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SEQ ID NO 2

LENGTH: 826
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                           Score 4325; I
                                                   Pred. No. 0;
0; Mismatches
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                                       100.0%;
100.0%;
                                                                    Conservative
Homo sapiens
                                                    1 Similarity
826; Conserv
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; ORGANISM: HC
US-09-988-687-2
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Best Local S:
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                        Prostate Cancer Sus
nd Orthologous Genes
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APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Pr.
TITLE OF INVENTION: Gene and a Paralog and
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT FILING DATE: 2001-11-20
PRIOR PRICATION NUMBER: 09/564,805
PRIOR FILING DATE: 2000-05-05
PRIOR PLILING DATE: 1908-11-06
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR PILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
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aralog and
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ilarity 98.9%;
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SEQ ID NO 224
LENGTH: 826
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US-09-988-626-224
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Sommers, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 1/P-Linked Prostate Cancer Susceptis
TITLE OF INVENTION: Chromosome 1/P-Linked Prostate Cancer Susceptis
TITLE OF INVENTION: 2018-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US/05-05
PRIOR APPLICATION NUMBER: US/05/05-05
PRIOR PLICATION NUMBER: US/05/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
SUSTWARE: Patentin Ver. 2.0
SEQ ID NO 224
LENGTH: 826
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Pred. No. 0;
4; Mismatches 5; Indels
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Publication No. US20030045704A1
GENERAL INFORMATION:
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Best Local Similarity 98.9%;
Matches 817; Conservative
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US-09-988-687-224
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181 YQIPIHSEQRRGRHQPWQSPERPLSRLSPERSSDSESNENEPHLPHGVSQRRGVRDSSLV 240
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LENGTH: 826
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Publication No. US20030044959A1

GENERAL INPORMATION:

APPLICANT: Tartigian, Sean V.

APPLICANT: Tartigian, Sean V.

APPLICANT: Tartigian, Sean V.

APPLICANT: APPLICANT: Acques

APPLICANT: Rommens, Johanna M.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

FILE REFERENCE: 2318-258

CURRENT APPLICATION NUMBER: US/09/988,626

CURRENT FILING DATE: 2001-11-20

PRIOR FILING DATE: 2000-05-05

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-11-05

NUMBER OF SEQ ID NOS: 240

SEQ ID NO 226

LENGTH: 826

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Best Local Similarity 98.5
Matches 814; Conservative
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US-09-988-626-226
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Publication No. US20030045704A1

GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Suscepti;
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: 09/564,805
PRIOR PLICATION NUMBER: 09/564,805
PRIOR PLICATION NUMBER: 09/544,382
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SEOFTAME: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 826;
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ERREKRELRQVRAALLSRELAGGLEDGEPQQKRAHTEE---PQAKK
                                                                                                                                             Matches 665;
                                                                             SEQ ID NO 222
LENGTH: 822
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Best Local 9
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Sequence 222. Application No. US20030044959A1

GENERAL INFORMATION:

APPLICANT: Tavitigian, Sean V.

APPLICANT: Tavitigian, Seau W.

APPLICANT: Sommens, Johanna M.

APPLICANT: Myriad Genetics, Inc.

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Chromosome and a Paralog and Orthologous Genes

FILE REFERENCE: 2318-258
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        Gaps
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                                MWALCSLLRSAAGRIMSQGRIISQAPARRERPRKDPLRHLRIREKRGPSGCSGGPNIVYL
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ed. No. 0;
Mismatches
Pred.
98.58;
      814; Conservative
Similarity
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Local
Best Loc
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Pred. No. 6.9e-294;
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    APPLICATION NUMBER: US/09/988,626
CURRENT APPLICATION NUMBER: US/09/988,6
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/564,805
PRIOR FILING DATE: 2000-05-05
PRIOR PELING DATE: 1008-10-06
PRIOR PELING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PALENTIN VET. 2.0
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ilarity 80.5%;
Conservative 60
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; ORGANISM: Mus musculus
US-09-988-626-222
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540 AAVFVSHLHADHHTGLPSILLQRERALASLGKPLHPLLVVAPNQLKAWLQQYHNQCQEVL
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LENGTH: 837
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                                                                                                                                       JAPPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Teng, David H.F.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Rowmens, Johanna M.
APPLICANT: Rowmens, Johanna M.
APPLICANT: Rowmens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: J118-28
CURRENT PLICATION NUMBER: US/09/988,687
CURRENT PLICATION NUMBER: 09/564,805
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR PLING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
COMPUTATION NUMBER: 09/434,382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9; Length 822;
80.3%; Score 3473.5; DB 9;
80.5%; Pred. No. 6.9e-294;
Live 66; Mismatches 76;
                                                                               S-09-988-687-222
Sequence 222, Application US/09988687
Publication No. US20030045704A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                : PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Mus musculus
US-09-988-687-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 665; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Pate
SEQ ID NO 222
LENGTH: 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION UNMBER: US/09/988,626
CURRENT FILING DATE: 2001-11-20
PRIOR PILING DATE: 1000-05-05
PRIOR PRILING DATE: 1998-11-06
PRIOR PILING DATE: 1998-11-06
PRIOR PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
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SGPLKGIEL-AVRPHSAPE---YEDETMTVYQI---PIHSEQRRGKHQPWQSPERPLSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 228, Application US/09988626; Publication No. US20030044959A1; GENERAL INFORMATION:
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Conservative 128;
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Sequence 228, Application US/09988687

Publication No. US20030045704A1

GENERAL INFORMATION:
APPLICANT: Tavitglan, Sean V.
APPLICANT: Tavitglan, Jacques
APPLICANT: Tavitglan, Jacques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION NUMBER: US/09/988,687

CURRENT FILING DATE: 2001-11-20

PRIOR FILING DATE: 2000-05-05

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-11-05

SOFTWARD PRIOR TILING DATE: 1999-11-05

SOFTWARD PRIOR TILING DATE: 1999-11-05
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                                                                                                                                                                                                                 579 VIVVGPRPLKRFLDAYQR-----LEDLDMEFLDCRSTTATSWASLESGGEAEGSLFTQGS
                              -----LNENCASVHNLRSHKIQTQLNLIHPDIFPLLTSFRCKKEGPTLSVPMVQG
                                                                                                      LLIIVSHQKTVRKNMAFPILKASSRIAARLNYLCPQFFPAPGFWPSQLTDNSIIDPTPSN
                                                                                                                                    ECLLKYQLRP--RREWQRDAIITCNPEEFIVEAL--QLPNFQQSVQEYRR--SAQDGPAP
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SEQ ID NO 228
LENGTH: 837
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  Gaps
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297; Indels 175;
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APPLICANT: Teng, David H.F.
APPLICANT: Simmard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
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; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/988,626
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: US/664,805
; PRIOR APPLICATION NUMBER: US/664,805
; PRIOR APPLICATION NUMBER: US/60/107,468
; PRIOR APPLICATION NUMBER: US/60/107,468
; PRIOR APPLICATION NUMBER: US/434,382
; PRIOR FILING DATE: 1998-11-05
; RIOR PRILING DATE: 1998-11-05
; SOFTYRARE: PALENTING DATE: 1999-11-05
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APPLICANT: Tany, David Hr. V.
APPLICANT: Tany, David Hr. V.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Sommens, Johnna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT FILING DATE: 2001-11-20
REIOR APPLICATION NUMBER: 09/564,805
PRIOR APPLICATION NUMBER: 09/564,805
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR PILING DATE: 1999-11-06
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver: 2.0
702 GKDADVLVHESTFEDGHEVDMTPKPPKKLAKISSLADAMRKRHSTMGQAVDVGKRMNAKH 761
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                                                                                           IMLNHFSQRYAKVPLFSPNF -- SEKVGVAFDHMKVCFGDFPTMPKLIPPLKALFAGDIEE
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 227, Application US/09988687; Publication No. US20030045704A1
GENERAL INFORMATION: APPLICANT: TAVLIGIAN, Sean V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT Caenorhabditis elegans US-09-988-687-227
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194	242	193 STNYEISESPVRGKFKVEEAIK 299 PPDPGAAFVVVECPDESFIQPI :::: :::	248 NERHFAKVLIL 359 ERFGPDTQHLV :	303	349	Db 409 EEPMKCNINGEVADFSWQEIFEEH-VKPI Qy 475 EKRSQYPEIIFLGTGSAIPMKINVSATI Db 462KKRHVFITTIGTGAIDSKYPNVSTI	527	OY 586 AWLQOYHNQCQEVLHHISMII	QY 657 SGWKVVXSGDTWPCEALVRMGKDATLI : : : 1 Db 691 T-FKVSXSGDTRPNIEKFSLEIGYNSDLI	QY 715 MNAEFIMLNHFSQRYAKVPLFSPNFR	Qy 772 AGDIEEMERREKRELRQVR 791 : : : :	RESULT 14 US-09-988-687-229 Sequence 229, Application US/099868; Publication No. US20030045704A1 GENERAL INFORMATION: APPLICANT: Tavitgian, Sean V. APPLICANT: Tenq, David H.F.	; APPLICANT: Simard, Jacques ; APPLICANT: Rommens, Johanna M. ; APPLICANT: Myriad Genetics, Inc. ; TITLE OF INVENTION: Chromosome 17p-1	; FILE REFERENCE: 218-258 ; CURRENT APPLICATION NUMBER: US/09/96 ; CURRENT FILING DATE: 2001-11-20 ; PRIOR APPLICATION NUMBER: 09/564,805 ; PRIOR APPLICATION NUMBER: US 60/107, PRIOR PELING DATE: 1998-11-06 ; PRIOR FILING DATE: 1998-11-0634,383
: : : : : : DWSGIITQNEELSQRQDQFIRVAPMQRYWMRRG-ASFNEEPIVNNLLAAEPELSDKAKE 467	Qy 459 SVQEYRRSAQDGPAPAEKRSQYPEIIFLGTGSAIPMKIRNVSATLVNISPDTSLLLDCGE 518	OY 519 GTFGQLCRHYG-DQVDRVLGTLAAVFVSHLHADHHTGLPSILLQRERALASLGKPLHPLL 577	QY 578 VVAPNQLKAMLQQYHNQCQEVLHHISMIPAKCLQEGAEISSP 619 1 :	QY 620AVERLISSL-LRTCDLEEFQTCLVRHCKHAFGCALVHTSGWKVVYSGDTMPCEALVRM 676 :: : : : :	QY 677 GKDATLLIHEATLEDGLE	Qy 720 IMLNHFSQRYAKVPLESPNFSEKVGVAFDHMKVCFGDFPTWPKLIPPLKALFAGDIEE 777	Oy 778 MEERREKRELR 788 :: : : Db 821 LTIKKEORVLK 831	RESULT 13 US-09-988-626-229 ; Sequence 229, Application US/09986626 ; Publication No. US20030044959A1 ; GENERAL INFORMATION: ; APPLICANT: Tavtigian, Sean V. ; APPLICANT: Tavtigian, Sean V.	APPLICANT: Sommens, Johanna M. APPLICANT: Myriad Genetics, Inc. TITLE OF INVENTION: Chromosome 170-Linked Prostate Cancer Susceptibility	; IIILE OF INVENTION: Gene and a Paralog and Orthologous Genes; FILE REFERENCE: 2318-258; CURRENT APPLICATION NUMBER: US/09/988,626; CURRENT FILING DATE: 2001-11-20; DIRECTOR APPLICATION NUMBER: OS/05-64.	FILE FILING DATE: 2000-05-05 PRIOR FILING DATE: 2000-05-05 PRIOR APPLICATION NUMBER: US 60/107,468 PRIOR FILING DATE: 1998-11-06 PRIOR PILING DATE: 1998-11-06 PRIOR FILING DATE: 1999-11-06	NUMBER OF SEQ ID NOS: 240 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 229 LENGTH: 838 TYPE: PRT ORGANISM: Saccharomyces cerevisiae US-09-988-626-229	Ouery Match 13.9%; Score 599.5; DB 9; Length 838; Best Local Similarity 25.7%; Pred. No. 2.8e-43; Matches 221; Conservative 138; Mismatches 290; Indels 211; Gaps 36;	QY 82 RYLF-NCGGGVQRLMQEHKLKVARLDNIFLT-RMHWSNVGGLSGMILTLKETGLPKCVLS 139 1

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LSIEYFQTCRAIHCDWAYSNSITFRMDENNEHN 690
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TLVKVPFTDADGNTINRNIMLDAGENTLGTIHR 519
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                            P--SSDPHLNVELPDL------DAKVEV 192
                                                               STAAIAPIIAAVKDGKSIT-HEGREILAEELCT 298
                                                                                    OTQLNLIHPDIFPL----LTSFRCK----- 406
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completed: May 14, 2003, 10:11:04
                          RESULT 15
US-09-988-626-211
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                                                                                                                                                                                                                                                                                                                                                         194 HQPWQS------PERPLSRLSPERSSDSESNENEPHLPHGVSQRRGVRDSSLVV 241
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                                                                                                                                                     Query Match 13.9%; Score 599.5; DB 9; Best Local Similarity 25.7%; Pred. No. 2.8e-43; Matches 221; Conservative 138; Mismatches 290;
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                                                                                                    ORGANISM: Saccharomyces cerevisiae US-09-988-687-229
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PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
                                                    SEQ ID NO 229
LENGTH: 838
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Taviijan, Sean V.

APPLICANT: Simard, Joqques

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

FILE REFERENCE: 2318-258

CURRENT APPLICATION NUMBER: US/09/988,626

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: US 60/107,468

PRIOR APPLICATION NUMBER: US 60/107,468

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-11-05

PRIOR FILING DATE: 1998-11-05

WUMBER OF SEQ ID NOS: 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.7%; Score 420; DB 9; 100.0%; Pred. No. 3.2e-29; Live 0; Mismatches 0;
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Matches 81; Conservative
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ORGANISM: Homo sapiens
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